

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:06 ; Search time 43.3077 Seconds
 (without alignments)
 71.766 Million cell updates/sec

Title: US-09-787-443A-21
 Perfect score: 11
 Sequence: 1 AKSRKGNSSLM 11

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22883

Minimum DB seq length: 11
 Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	11	100.0	11	3	AAY88549	Aay88549 NCAM Igl
2	11	100.0	11	5	ABG69349	Abg69349 Human neu
3	4	36.4	11	2	AAR04739	Aar04739 Deduced s
4	4	36.4	11	2	AAY07532	Aay07532 Laminin-d
5	4	36.4	11	2	AAY07531	Aay07531 Laminin-d
6	4	36.4	11	2	AAW76689	Aaw76689 Plasmid p
7	4	36.4	11	4	AAM98749	Aam98749 Human pep
8	4	36.4	11	4	AAB68771	Aab68771 Human FAS
9	4	36.4	11	4	ABP17604	Abp17604 HIV B58 s

10	4	36.4	11	5	ABB74319	Abb74319 Simple nu
11	4	36.4	11	6	ABP99717	Abp99717 Human sec
12	4	36.4	11	6	ABP72546	Abp72546 Peptide e
13	4	36.4	11	6	ABR01199	Abr01199 Human gen
14	4	36.4	11	7	ADC22397	Adc22397 Nuclear l
15	3	27.3	11	1	AAP50987	Aap50987 FTS-deriv
16	3	27.3	11	1	AAP50941	Aap50941 Hepatitis
17	3	27.3	11	1	AAP82901	Aap82901 Activated
18	3	27.3	11	1	AAP80854	Aap80854 Sequence
19	3	27.3	11	1	AAP81302	Aap81302 Atrial na
20	3	27.3	11	2	AAY07371	Aay07371 Matrix me
21	3	27.3	11	2	AAR07165	Aar07165 Synthetic
22	3	27.3	11	2	AAR10045	Aar10045 N-termina
23	3	27.3	11	2	AAR14094	Aar14094 Pre-S(1-1
24	3	27.3	11	2	AAR44308	Aar44308 Ballast c
25	3	27.3	11	2	AAR31358	Aar31358 Antimicro
26	3	27.3	11	2	AAR24850	Aar24850 Weight re
27	3	27.3	11	2	AAR28088	Aar28088 Cell-to-c
28	3	27.3	11	2	AAR25763	Aar25763 Histone H
29	3	27.3	11	2	AAR27520	Aar27520 Effector
30	3	27.3	11	2	AAR26085	Aar26085 Immunisin
31	3	27.3	11	2	AAR26084	Aar26084 Immunisin
32	3	27.3	11	2	AAR26832	Aar26832 TY-11(6)
33	3	27.3	11	2	AAR26834	Aar26834 CY-11(8)
34	3	27.3	11	2	AAR26833	Aar26833 CY-11(7)
35	3	27.3	11	2	AAR26835	Aar26835 CY-11(9)
36	3	27.3	11	2	AAR36904	Aar36904 Insulin-l
37	3	27.3	11	2	AAR36924	Aar36924 Insulin-l
38	3	27.3	11	2	AAR36905	Aar36905 Insulin-l
39	3	27.3	11	2	AAR36894	Aar36894 Insulin-l
40	3	27.3	11	2	AAR36917	Aar36917 Insulin-l
41	3	27.3	11	2	AAR36874	Aar36874 Insulin-l
42	3	27.3	11	2	AAR36914	Aar36914 Insulin-l
43	3	27.3	11	2	AAR42959	Aar42959 Beta chai
44	3	27.3	11	2	AAR42956	Aar42956 Beta chai
45	3	27.3	11	2	AAR32352	Aar32352 Human Fac
46	3	27.3	11	2	AAR43594	Aar43594 Peptide d
47	3	27.3	11	2	AAR43598	Aar43598 Peptide d
48	3	27.3	11	2	AAR43618	Aar43618 Peptide d
49	3	27.3	11	2	AAR43599	Aar43599 Peptide d
50	3	27.3	11	2	AAR43638	Aar43638 Peptide d
51	3	27.3	11	2	AAR37430	Aar37430 Promega p
52	3	27.3	11	2	AAR44560	Aar44560 Encoded b
53	3	27.3	11	2	AAR53641	Aar53641 Mutant tr
54	3	27.3	11	2	AAR52885	Aar52885 TK-SH2 as
55	3	27.3	11	2	AAR52886	Aar52886 TK-SH2 as
56	3	27.3	11	2	AAR68593	Aar68593 Rat NDF p
57	3	27.3	11	2	AAR78518	Aar78518 Synthetic
58	3	27.3	11	2	AAW21497	Aaw21497 Hepatitis
59	3	27.3	11	2	AAW21210	Aaw21210 Farnesyl
60	3	27.3	11	2	AAR98482	Aar98482 Anti-IL-5
61	3	27.3	11	2	AAW05770	Aaw05770 Presenili
62	3	27.3	11	2	AAR89702	Aar89702 Prostate
63	3	27.3	11	2	AAR89705	Aar89705 Prostate
64	3	27.3	11	2	AAR98513	Aar98513 CD8 antag
65	3	27.3	11	2	AAW06895	Aaw06895 Anti-CD18
66	3	27.3	11	2	AAR91286	Aar91286 Anti-idio

67	3	27.3	11	2	AAW09653	Aaw09653	Labelled
68	3	27.3	11	2	AAE22529	Aae22529	Human Fcg
69	3	27.3	11	2	AAW11502	Aaw11502	Humanised
70	3	27.3	11	2	AAW44188	Aaw44188	H-2Kd-res
71	3	27.3	11	2	AAW11511	Aaw11511	Humanised
72	3	27.3	11	2	AAW30194	Aaw30194	Salvage r
73	3	27.3	11	2	AAW15672	Aaw15672	Platelet
74	3	27.3	11	2	AAW25009	Aaw25009	Oncoimmun
75	3	27.3	11	2	AAW28862	Aaw28862	HTLV-1a,c
76	3	27.3	11	2	AAW24059	Aaw24059	Salvage r
77	3	27.3	11	2	AAW15948	Aaw15948	Interleuk
78	3	27.3	11	2	AAW27332	Aaw27332	Salvage r
79	3	27.3	11	2	AAW33597	Aaw33597	Oligopept
80	3	27.3	11	2	AAW33539	Aaw33539	Oligopept
81	3	27.3	11	2	AAW33536	Aaw33536	Oligopept
82	3	27.3	11	2	AAW33583	Aaw33583	Oligopept
83	3	27.3	11	2	AAW41012	Aaw41012	Anti-glut
84	3	27.3	11	2	AAW34507	Aaw34507	Salvage r
85	3	27.3	11	2	AAW65652	Aaw65652	Peptide #
86	3	27.3	11	2	AAW62364	Aaw62364	Antithrom
87	3	27.3	11	2	AAW42459	Aaw42459	Mouse ant
88	3	27.3	11	2	AAW57427	Aaw57427	Amino aci
89	3	27.3	11	2	AAW68880	Aaw68880	Peptide b
90	3	27.3	11	2	AAW59349	Aaw59349	Human Fab
91	3	27.3	11	2	AAW72876	Aaw72876	Bacillus
92	3	27.3	11	2	AAW40511	Aaw40511	Mouse ner
93	3	27.3	11	2	AAW40510	Aaw40510	Human ner
94	3	27.3	11	2	AAW62020	Aaw62020	Salvage r
95	3	27.3	11	2	AAW20426	Aay20426	Human mic
96	3	27.3	11	2	AAW54632	Aaw54632	Peptide f
97	3	27.3	11	2	AAW70627	Aaw70627	Salvage r
98	3	27.3	11	2	AAW37137	Aaw37137	Cyclic pi
99	3	27.3	11	2	AAW40573	Aaw40573	Human IgG
100	3	27.3	11	2	AAW44819	Aaw44819	Salvage r

ALIGNMENTS

RESULT 1

AAW88549

ID AAW88549 standard; peptide; 11 AA.

XX

AC AAW88549;

XX

DT 07-AUG-2000 (first entry)

XX

DE NCAM Igl binding peptide #21.

XX

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;

KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;

KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW treatment; prosthetic nerve guide; treatment; nervous system.

XX

OS Synthetic.

XX

PN WO200018801-A2.
XX
PD 06-APR-2000.
XX
PF 23-SEP-1999; 99WO-DK000500.
XX
PR 29-SEP-1998; 98DK-00001232.
PR 29-APR-1999; 99DK-00000592.
XX
PA (RONN/) RONN L C B.
PA (BOCK/) BOCK E.
PA (HOLM/) HOLM A.
PA (OLSE/) OLSEN M.
PA (OSTE/) OSTERGAARD S.
PA (JENS/) JENSEN P H.
PA (POUL/) POULSEN F M.
PA (SORO/) SOROKA V.
PA (RALE/) RALETS I.
PA (BERE/) BEREZIN V.
XX
PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX
DR WPI; 2000-293111/25.
XX
PT Compositions that bind neural cell adhesion molecules useful for treating
PT disorders of the nervous system and muscles e.g. Alzheimer's and
PT Parkinson's diseases.
XX
PS Example 4; Page 25; 119pp; English.
XX
CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
CC NCAM is found in three forms, two of which are transmembrane forms, while
CC the third is attached via a lipid anchor to the cell membrane. All three
CC NCAM forms have an extracellular structure consisting five immunoglobulin
CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-
CC terminal. The present sequence represents a peptide which binds to the
CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
CC outgrowth from NCAM presenting cells, and is also capable of promoting
CC the proliferation of NCAM presenting cells. The compound may be used in
CC the treatment of normal, degenerated or damaged NCAM presenting cells.
CC The compound may in particular be used to treat diseases of the central
CC and peripheral nervous systems such as post-operative nerve damage,
CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
CC dementias, sclerosis, nerve degeneration associated with diabetes
CC mellitus, disorders affecting the circadian clock or neuro-muscular
CC transmission and schizophrenia. Conditions affecting the muscles may also
CC be treated with the compound, such as conditions associated with impaired
CC function of neuromuscular connections (e.g. genetic or traumatic shock or
CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
CC liver and bowel may also be treated using the compound. The compound is
CC used in a prosthetic nerve guide, and also to stimulate the ability to
CC learn, and to stimulate the memory of a subject
XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.4e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKSRKGNSSLM 11
| | | | | | | | | |
Db 1 AKSRKGNSSLM 11

RESULT 2

ABG69349

ID ABG69349 standard; peptide; 11 AA.

XX

AC ABG69349;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human neural cell adhesion molecule (NCAM) peptide #21.

XX

KW Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;

KW acute myocardial infarction; central nervous system disorder; stroke;

KW peripheral nervous system disorder; postoperative nerve damage;

KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;

KW postischaemic damage; multiinfarct dementia; multiple sclerosis;

KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;

KW Alzheimer's disease; Parkinson's disease;

KW Huntington's disease. atrophic muscle disorder; gonad degeneration;

KW nephrosis.

XX

OS Homo sapiens.

XX

PN WO200247719-A2.

XX

PD 20-JUN-2002.

XX

PF 12-DEC-2001; 2001WO-DK000822.

XX

PR 12-DEC-2000; 2000DK-00001863.

XX

PA (ENKA-) ENKAM PHARM AS.

XX

PI Bock E, Berezin V, Kohler LB;

XX

DR WPI; 2002-583473/62.

XX

PT Use of a compound comprising a peptide of neural cell adhesion molecule,
PT in the preparation of medicament for preventing death of cells presenting
PT NCAM or NCAM ligand and treating central nervous system diseases.

XX

PS Disclosure; Page 16; 57pp; English.

XX

CC The invention relates to use of a compound (I) comprising a peptide which
CC comprises at least 5 contiguous amino acid residues of a sequence of the
CC neural cell adhesion molecule (NCAM), its fragment, variant or its mimic,
CC for the preparation of a medicament for preventing death of cells

CC presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
 CC of a medicament for preventing death of cells presenting the NCAM or an
 CC NCAM ligand. The medicament is for the stimulation of the survival of
 CC heart muscle cells, such as survival after acute myocardial infarction.
 CC The medicament is for the treatment of diseases or conditions of the
 CC central and peripheral nervous system, such as postoperative nerve
 CC damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
 CC impaired myelination of nerve fibres, postischaemic damage, e.g.
 CC resulting from a stroke, multiinfarct dementia, multiple sclerosis, nerve
 CC degeneration associated with diabetes mellitus, neuro-muscular
 CC degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and
 CC Huntington's disease. The medicament is for the treatment of diseases or
 CC conditions of the muscles including conditions with impaired function of
 CC neuro-muscular connections, such as genetic or traumatic atrophic muscle
 CC disorders, and for the treatment of diseases or conditions of various
 CC organs, such as degenerative conditions of the gonads, pancreas (e.g.
 CC diabetes mellitus type I and II) and kidney (e.g. nephrosis). ABG69329-
 CC ABG69352 represent human NCAM peptides of the invention
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.4e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKSRKGNSSLM 11
 |||||
 Db 1 AKSRKGNSSLM 11

RESULT 3

AAR04739

ID AAR04739 standard; protein; 11 AA.

XX

AC AAR04739;

XX

DT 31-OCT-2002 (revised)

DT 05-AUG-1990 (first entry)

XX

DE Deduced sequence at fusion point of E. coli lacZ and Cellulomonas fimi
 DE endoglucanase (CenA) in expression plasmid pUCEC2.

XX

KW LacZ-endoglucanase expression plasmid pUCEC2; CenA;

~~KW Cellulomonas fimi-endoglucanase.~~

XX

OS Cellulomonas fimi.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Protein	1..6
----	---------	------

FT		/note= "lacZ"
----	--	---------------

FT	Protein	7..11
----	---------	-------

FT		/note= "CenA"
----	--	---------------

XX

PN WO9000609-A.

XX

PD 25-JAN-1990.

XX

PF 28-JUN-1989; 89WO-GB000718.
 XX
 PR 08-JUL-1988; 88US-00216794.
 XX
 PA (UYBR-) UNIV BRIT COLUMBIA.
 XX
 PI Kilburn DG, Miller RC, Warren RA, Gilkes NR;
 XX
 DR WPI; 1990-051713/07.
 DR N-PSDB; AAQ02961.
 XX
 PT Polysaccharide matrix bonded with fusion protein - contg.
 PT polysaccharidase binding region and specific polypeptide, useful for
 PT affinity purificn. and immobilisation, e.g. for drug delivery.
 XX
 PS Example 2; Fig 4B; 47pp; English.
 XX
 CC A 1.6 kb fragment from the 6.0 kb insert of C. fimi DBA in pCEC2 was
 CC purified and sub-cloned into the SstI site of pUC18 to form pUCEC2. It is
 CC constructed to illustrate method of preparation of a polysaccharide
 CC matrix bonded to a hybrid protein and a substrate binding region (SBR) of
 CC a polysaccharidase. The binding of the hybrid protein to the matrix is a
 CC rapid and inexpensive method of purifying it. (Updated on 31-OCT-2002 to
 CC add missing OS field.)
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSLM 11
 ||||
 Db 7 SSLM 10

RESULT 4
 AAY07532

ID AAY07532 standard; peptide; 11 AA.

XX

AC AAY07532;

XX

DT 17-AUG-1999 (first entry)

XX

DE Laminin-derived peptide linked to metal-binding domain.

XX

KW Laminin; diagnostic; metal-binding; polyvalent; linked; branched; repeat;
 KW platelet accumulation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Domain 1. .5

FT /label= Biological_function

FT /note= "Laminin-derived peptide"

FT Modified-site 1

FT /note= "N-acetyl-Tyr"

FT Modified-site 6
 FT /note= "The epsilon-amino group of this residue has
 FT another biological function domain of formula Ac-YIGSR-
 FT attached to it"
 FT Domain 7. .11
 FT /label= Metal_ion-binding
 FT Misc-difference 10
 FT /note= "D-form residue"
 FT Modified-site 11
 FT /note= "Gly-NH2"
 XX
 PN WO9501188-A1.
 XX
 PD 12-JAN-1995.
 XX
 PF 01-JUL-1994; 94WO-US007462.
 XX
 PR 02-JUL-1993; 93US-00087219.
 PR 30-JUN-1994; 94US-00269929.
 XX
 PA (RHOM-) RHOMED INC.
 XX
 PI Rhodes BA, Zamora PO, Freer RJ, Sharma SD;
 XX
 DR WPI; 1995-060818/08.
 XX
 PT New high affinity peptide-based compsns. for diagnosis and therapy - in
 PT which peptide has at least two biological-functional domains and a metal
 PT ion binding domain.
 XX
 PS Disclosure; Page 42; 60pp; English.
 XX
 CC The patent discloses a high affinity peptide-based pharmaceutical
 CC composition which comprises (a) at least two linear repeat, linked or
 CC branched amino acid sequence biological-function domains and (b) one or
 CC more medically useful metal ion-binding domains. When bound with a
 CC medically useful metal (e.g. an isotope of Tc, Re, In, Au, Ag, Hg or Cu),
 CC the composition can be used for detection and treatment of pathological
 CC conditions and for diagnostic imaging. The composition allows direct
 CC binding with a metal without the necessity of conjugation to bifunctional
 CC chelators. Metals can be bound while retaining the high activity of the
 CC biological function domains. The present sequence represents a laminin-
 CC derived peptide (a preferred example of a biological function domain)
 CC joined to a metal ion binding domain via a Lys residue which has another
 CC laminin-derived peptide attached to its side chain amino group. Metal-
 CC bound compositions containing the sequence can be used for detection of
 CC sites of platelet accumulation in e.g. thrombosis, pulmonary embolism,
 CC inflammatory response secondary to myocardial infarction, endocarditis,
 CC bypass graft occlusion, aneurysms, prosthetic arterial graft platelet
 CC accumulation, prosthetic arterial graft platelet occlusion, cerebral
 CC embolism, cerebral haemorrhage, traumatic injury with haemorrhage,
 CC gastrointestinal haemorrhage and thrombosis secondary to catheters and
 CC other implanted devices, or for detection of carcinomas including primary
 CC carcinomas and metastatic carcinomas
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRKG 6
||||
Db 4 SRKG 7

RESULT 5

AAY07531

ID AAY07531 standard; peptide; 11 AA.

XX

AC AAY07531;

XX

DT 17-AUG-1999 (first entry)

XX

DE Laminin-derived peptide linked to metal-binding domain.

XX

KW Laminin; diagnostic; metal-binding; polyvalent; linked; branched; repeat;
KW platelet accumulation.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Domain 1. .5

FT /label= Biological_function

FT /note= "Laminin-derived peptide"

FT Modified-site 1

FT /note= "N-acetyl-Tyr"

FT Modified-site 6

FT /note= "The epsilon-amino group of this residue has
FT another biological function domain of formula Ac-YIGSR-
FT attached to it"

FT Domain 7. .11

FT /label= Metal_ion-binding

FT Modified-site 11

FT /note= "Ala-NH2"

XX

PN WO9501188-A1.

XX

PD 12-JAN-1995.

XX

PF 01-JUL-1994; 94WO-US007462.

XX

PR 02-JUL-1993; 93US-00087219.

PR 30-JUN-1994; 94US-00269929.

XX

PA (RHOM-) RHOMED INC.

XX

PI Rhodes BA, Zamora PO, Freer RJ, Sharma SD;

XX

DR WPI; 1995-060818/08.

XX

PT New high affinity peptide-based compsns. for diagnosis and therapy - in
PT which peptide has at least two biological-functional domains and a metal
PT ion binding domain.

XX
 PS Disclosure; Page 42; 60pp; English.
 XX
 CC The patent discloses a high affinity peptide-based pharmaceutical
 CC composition which comprises (a) at least two linear repeat, linked or
 CC branched amino acid sequence biological-function domains and (b) one or
 CC more medically useful metal ion-binding domains. When bound with a
 CC medically useful metal (e.g. an isotope of Tc, Re, In, Au, Ag, Hg or Cu),
 CC the composition can be used for detection and treatment of pathological
 CC conditions and for diagnostic imaging. The composition allows direct
 CC binding with a metal without the necessity of conjugation to bifunctional
 CC chelators. Metals can be bound while retaining the high activity of the
 CC biological function domains. The present sequence represents a laminin-
 CC derived peptide (a preferred example of a biological function domain)
 CC joined to a metal ion binding domain via a Lys residue which has another
 CC laminin-derived peptide attached to its side chain amino group. Metal-
 CC bound compositions containing the sequence can be used for detection of
 CC sites of platelet accumulation in e.g. thrombosis, pulmonary embolism,
 CC inflammatory response secondary to myocardial infarction, endocarditis,
 CC bypass graft occlusion, aneurysms, prosthetic arterial graft platelet
 CC accumulation, prosthetic arterial graft platelet occlusion, cerebral
 CC embolism, cerebral haemorrhage, traumatic injury with haemorrhage,
 CC gastrointestinal haemorrhage and thrombosis secondary to catheters and
 CC other implanted devices, or for detection of carcinomas including primary
 CC carcinomas and metastatic carcinomas
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SRKG 6
 ||||
 Db 4 SRKG 7

RESULT 6
 AAW76689

ID AAW76689 standard; protein; 11 AA.

XX

AC AAW76689;

XX

DT 05-JAN-1999 (first entry)

XX

DE Plasmid pGEX-3X protein fragment.

XX

KW Dendroaspin; snake venom; clotting cascade; anticoagulant; platelet;
 KW integrin binding; injury; blood; cell migration; thrombosis; inhibitor;
 KW proliferation; signal transduction; regulator; coagulation; treatment;
 KW prophylactic; artery; vein; wall thickening; myocardial infarction;
 KW retinal neovascularisation; dysregulated apoptosis; tumorigenesis;
 KW leukocyte recruitment, immune system; tissue fibrosis.

XX

OS Synthetic.

XX

PN WO9842834-A1.

XX
 PD 01-OCT-1998.
 XX
 PF 20-MAR-1998; 98WO-GB000848.
 XX
 PR 20-MAR-1997; 97GB-00005787.
 XX
 PA (THRO-) THROMBOSIS RES INST.
 XX
 PI Lu X, Scully MF, Kakkar V, Authi K;
 XX
 DR WPI; 1998-542278/46.
 DR N-PSDB; AAV61951.
 XX
 PT New hybrid dendroaspin polypeptide(s) - used for treating, e.g.
 PT thrombosis, myocardial infarction, dysregulated apoptosis, abnormal cell
 PT migration and immune system activation.
 XX
 PS Example 2; Fig 4; 59pp; English.
 XX
 CC This sequence represents a fragment of the plasmid pGEX-3X which is used
 CC in the isolation of a snake venom dendroaspin fragment. When dendroaspin
 CC is modified to incorporate further functional amino acid sequence, e.g.
 CC active portions or motifs of agonists, antagonists or inhibitors of
 CC factors in the clotting cascade, the resulting molecules are particularly
 CC useful as anticoagulants. The molecules have an integrin binding activity
 CC which when administered in vivo results in the binding of the molecules
 CC to platelets thereby inhibiting the aggregation of the platelets at sites
 CC of injury. Non-wild type dendroaspin domains provide secondary,
 CC optionally further functionality, e.g. antithrombotic action, inhibiting
 CC cell migration and proliferation and regulating signal transduction. Such
 CC variants have bi- or multifunctional activities against blood
 CC coagulation, particularly thrombus formation and arterial/venous wall
 CC thickening at the sites of injury. The variants may have activities
 CC against leukocyte recruitment, immune system activation, tissue fibrosis
 CC and tumourigenesis. The polypeptides can be used for the treatment or
 CC prophylaxis of a disease associated with thrombosis, e.g. myocardial
 CC infarction, retinal neovascularisation, endothelial injury, dysregulated
 CC apoptosis, abnormal cell migration, leukocyte recruitment, immune system
 CC activation, tissue fibrosis or tumorigenesis
 XX
 SQ Sequence 11 AA;

Query-Match 36.4%; Score 4; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GNSS 9
 ||||
 Db 8 GNSS 11

RESULT 7
 AAM98749
 ID AAM98749 standard; peptide; 11 AA.
 XX
 AC AAM98749;

XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human peptide #2024 encoded by a SNP oligonucleotide.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US035498.
 XX
 PR 28-DEC-1999; 99US-0173419P.
 PR 27-DEC-2000; 2000US-00173419.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI; 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.
 XX
 PS Disclosure; Page 4112; 4143pp; English.
 XX
 CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC ~~The present sequence is a peptide encoded by one such oligonucleotide.~~
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms
 XX
 SQ Sequence 11 AA;

Query Match

36.4%; Score 4; DB 4; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSIM 11
||||
Db 7 SSIM 10

RESULT 8

AAB68771

ID AAB68771 standard; peptide; 11 AA.

XX

AC AAB68771;

XX

DT 18-APR-2001 (first entry)

XX

DE Human FAS peptide #1.

XX

KW Human; fatty acid synthase; FAS; polyketide synthase;

KW ketoacyl synthase domain; decarboxylation; polyketide synthase priming.

XX

OS Homo sapiens.

XX

PN WO200104274-A2.

XX

PD 18-JAN-2001.

XX

PF 06-JUL-2000; 2000WO-US018494.

XX

PR 07-JUL-1999; 99US-00348974.

XX

PA (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.

XX

PI Smith S, Joshi A, Rangan V, Witkowski A;

XX

DR WPI; 2001-138335/14.

XX

PT Novel polyketide synthase with improved and enhanced priming, generated

PT by incorporating a ketoacyl synthase domain with increased

PT decarboxylative activity into loading module of polyketide synthase.

XX

PS Disclosure; Fig 1A; 39pp; English.

XX

~~CC The present sequence is given in a specification relating to a novel~~
CC polyketide synthase with improved and enhanced priming. The polyketide
CC synthase was generated by incorporating a ketoacyl synthase domain with
CC increased decarboxylative activity into a loading module of polyketide
CC synthase. The loading module comprises an acyl carrier protein, an acyl
CC transferase domain and a ketoacyl synthase domain variant with a non-
CC nucleophilic residue at the position corresponding to residue 161 in the
CC rat fatty acid synthase. The ketoacyl synthase domain has increased
CC decarboxylase activity by mutation of a conserved active site cysteine
CC residue corresponding to residue 161 in rat fatty acid synthase. The
CC ketoacyl synthase domains with enhanced decarboxylation activity improve
CC priming or loading of polyketide synthases

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSIM 11
| | | |
Db 7 SSIM 10

RESULT 9

ABP17604

ID ABP17604 standard; peptide; 11 AA.

XX

AC ABP17604;

XX

DT 11-SEP-2003 (revised)

DT 15-JUL-2002 (first entry)

XX

DE HIV B58 super motif env peptide #5.

XX

KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;

KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;

KW vaccine; HIV infection; immunisation; virucide.

XX

OS Human immunodeficiency virus 1.

XX

PN WO200124810-A1.

XX

PD 12-APR-2001.

XX

PF 05-OCT-2000; 2000WO-US027766.

XX

PR 05-OCT-1999; 99US-00412863.

XX

PA (EPIM-) EPIMMUNE INC.

XX

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;

PI Baker DM, Celis E, Kubo RT, Grey HM;

XX

DR WPI; 2001-354887/37.

XX

PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)

PT peptide groups, useful for vaccinating against HIV-1.

XX

PS Claim 32; Page 230; 448pp; English.

XX

CC The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may

CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,

CC particularly when compared to the use of whole antigens in vaccine

CC compositions. There is evidence that the immune response to whole

CC antigens is directed largely toward variable regions of the antigen,

CC allowing for immune escape due to mutations. The groups for inclusion in

CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GNSS 9

||||

Db 4 GNSS 7

RESULT 10

ABB74319

ID ABB74319 standard; peptide; 11 AA.

XX

AC ABB74319;

XX

DT 18-APR-2002 (first entry)

XX

DE Simple nuclear localisation signal peptide SEQ ID NO:83.

XX

KW Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;

KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;

KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;

KW breast carcinoma; prostate carcinoma.

XX

OS Synthetic.

XX

PN WO200193836-A2.

XX

PD 13-DEC-2001.

XX

PF 08-JUN-2001; 2001WO-US018657.

XX

PR 09-JUN-2000; 2000US-0210925P.

XX

PA (BOUL/) BOULIKAS T.

XX

PI Boulikas T;

XX

DR WPI; 2002-164295/21.

XX

PT Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with

PT nuclear localization signal/fusogenic peptide conjugates into targeted

PT liposome complexes.

XX

PS Claim 14; Page 57; 107pp; English.

XX

CC The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on
CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC for delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic
CC and antitumour activities. The peptide-lipid-polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated
CC molecules display therapeutic efficacy in eradicating solid tumours
CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABB74235 to ABB74255 are used in the exemplification of the present
CC invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRKG 6

||||

Db 4 SRKG 7

RESULT 11

ABP99717

ID ABP99717 standard; protein; 11 AA.

XX

AC ABP99717;

XX

DT 26-MAR-2003 (first entry)

XX

DE Human secreted protein SEQ ID NO 661.

XX

KW Human; secreted protein; nootropic; neuroprotective; cytostatic;
KW virucide; dermatological; immunosuppressive; antiinflammatory; anti-HIV;
KW vulnerary; antibacterial; antiparkinsonian; antisickling; antianaemic;
KW antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective;
KW antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant;
KW antifungal; antiparasitic; cardiant; immune disorder; infection; vaccine;
KW cardiovascular disorder; neurological disease; nephrotropic;
KW gene therapy.

XX

OS Homo sapiens.

XX
 PN WO200277186-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009188.
 XX
 PR 27-MAR-2001; 2001US-0278650P.
 PR 12-SEP-2001; 2001US-00950082.
 PR 12-SEP-2001; 2001US-00950083.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI; 2003-040583/03.
 DR N-PSDB; ABZ67138.
 XX
 PT New human secreted proteins encoded by genes contained in cDNA clones
 PT (e.g. HGCAC19), useful for preventing, treating or diagnosing e.g. AIDS,
 PT multiple sclerosis, herpes virus, leukemia, tick-borne encephalitis or
 PT West Nile fever.
 XX
 PS Claim 1; Page 1462; 2423pp; English.
 XX
 CC The invention relates to novel human genes (ABZ66891-ABZ68209) and the
 CC encoded secreted proteins (ABP99470-ABP99872) useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The genes are isolated from a range of human tissues disclosed
 CC in the specification. The nucleic acids, proteins, antibodies and
 CC (ant)agonists are useful in the diagnosis, treatment and prevention of:
 CC (a) cancer, e.g. breast and ovarian cancer and other cancers of the
 CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
 CC lung or urogenital; (b) immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
 CC myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.
 CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
 CC bacterial, fungal and parasitic infections
 XX
 SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSM 11
 ||||
 Db 3 SSM 6

RESULT 12
 ABP72546
 ID ABP72546 standard; peptide; 11 AA.
 XX
 AC ABP72546;

XX
 DT 29-MAY-2003 (first entry)
 XX
 DE Peptide encoded by cloning region of vector pGEX-3X.
 XX
 KW Vector; pGEX-3X; vasoactive intestinal peptide; bombesin; substance P;
 KW epidermal growth factor; human; cancer; vaccine.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Cleavage-site 1. .4
 FT /note= "Factor Xa cleavage site"
 XX
 PN WO2003013426-A2.
 XX
 PD 20-FEB-2003.
 XX
 PF 02-AUG-2002; 2002WO-US024561.
 XX
 PR 03-AUG-2001; 2001US-0309975P.
 XX
 PA (DABU-) DABUR RES FOUND.
 PA (CORD/) CORD J I.
 XX
 PI Mukherjee R, Rao MRS, Burman AC, Thomas B, Prasad S, Sengupta P;
 XX
 DR WPI; 2003-256477/25.
 DR N-PSDB; ABZ81613.
 XX
 PT New multivalent vaccine comprising vasoactive intestinal peptide,
 PT Bombesin, Substance P and epidermal growth factor peptides, useful for
 PT preventing or treating cancer.
 XX
 PS Example 2; Fig 5; 6lpp; English.
 XX
 CC The present sequence is the peptide encoded by the cloning/expression
 CC region of vector plasmid pGEX-3X. This prokaryotic expression vector
 CC provides protein expression as a C-terminal fusion with glutathione
 CC transferase, which enables purification of the protein on a glutathione-
 CC Sepharose column. In the present invention, the target gene for cloning
 CC was a synthetic gene (see ABZ70689) encoding a multivalent polypeptide
 CC (see ABP72533) comprising vasoactive intestinal peptide, bombesin,
 CC substance P and epidermal growth factor joined via glycine-glycine
 CC linkers. This is useful as a multivalent vaccine for the prevention and
 CC treatment of e.g. colon, rectum, lung, breast, brain, pancreas, prostate,
 CC liver, gastrointestinal, thyroid, ovary, head and neck, and kidney
 CC cancers, melanoma, neuroblastoma, glioblastoma, leukaemia and lymphoma
 XX
 SQ Sequence 11 AA;

 Query Match 36.4%; Score 4; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 GNSS 9
 ||||

RESULT 13

ABR01199

ID ABR01199 standard; peptide; 11 AA.

XX

AC ABR01199;

XX

DT 12-MAY-2003 (first entry)

XX

DE Human gene 253-encoded secreted protein HOUED72, SEQ ID NO:680.

XX

KW Human; secreted protein; cancer; tumour; hyperproliferative disorder;
KW autoimmune disorder; inflammation; angiogenic diseases; AIDS;
KW acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing;
KW drug screening; chromosome identification; chromosome mapping;
KW cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV;
KW antianaemic; vulnerary.

XX

OS Homo sapiens.

XX

PN WO200277013-A2.

XX

PD 03-OCT-2002.

XX

PF 26-MAR-2002; 2002WO-US009370.

XX

PR 27-MAR-2001; 2001US-0278650P.

PR 12-SEP-2001; 2001US-00950082.

PR 12-SEP-2001; 2001US-00950083.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ruben SM;

XX

DR WPI; 2003-040578/03.

DR N-PSDB; ABZ73533.

XX

PT New human secreted proteins and nucleic acids, useful for detecting or
PT treating cancer or other hyperproliferative disorders, autoimmune
PT disorders, inflammatory disorders, HIV disease, hepatitis or anemia.

XX

PS ~~Claim 13; Page 1460; 2474pp; English.~~

XX

CC ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted
CC protein genes, and ABP00947-ABP01363 represent the proteins they encode.
CC ABZ73698-ABZ74687 represent human secreted protein genomic fragments. The
CC invention also encompasses antibodies specific for the secreted proteins,
CC the use of the secreted proteins in drug screening and recombinant
CC vectors and host cells comprising a nucleic acid of the invention. The
CC secreted proteins are thought to be involved in biological activities
CC associated with cellular signalling, cellular differentiation, cell
CC migration, prohormone activation and neurotransmitter activity. The
CC secreted proteins, nucleic acids encoding them, antibodies or antibody
CC fragments specific for the secreted proteins, and modulators of protein
CC activity are useful for diagnosing or treating cancers or other

CC hyperproliferative disorders. Additionally, the secreted proteins and
CC their nucleic acids may also be used in the treatment of autoimmune
CC disorders, inflammatory disorders, diseases involving angiogenesis, AIDS
CC (acquired immunodeficiency syndrome), hepatitis, anaemia, and to promote
CC wound healing. Nucleic acids of the invention may be used for chromosome
CC identification, chromosome mapping, in gene therapy, for identifying
CC individuals from minute biological samples, as hybridisation probes, and
CC as molecular weight markers. The present sequence represents a human
CC secreted protein of the invention

XX

SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSLM 11

||||

Db 3 SSLM 6

RESULT 14

ADC22397

ID ADC22397 standard; peptide; 11 AA.

XX

AC ADC22397;

XX

DT 18-DEC-2003 (first entry)

XX

DE Nuclear localisation signal motif amino acid sequence SEQ ID NO:246.

XX

KW recombinant fusion protein; fusion protein; binding; detection;

KW localisation domain; binding domain;

KW subcellular compartment localisation.

XX

OS Unidentified.

XX

PN WO2003012068-A2.

XX

PD 13-FEB-2003.

XX

PF 01-AUG-2002; 2002WO-US024572.

XX

PR 01-AUG-2001; 2001US-0309395P.

PR 13-DEC-2001; 2001US-0341589P.

XX

PA (CELL-) CELLOMICS INC.

XX

PI Bright G, Premkumar DR, Chen Y;

XX

DR WPI; 2003-248174/24.

XX

PT New recombinant fusion protein comprising detection and first

PT localization domains and a binding domain for the molecule of interest,

PT useful for detecting binding of a molecule of interest.

XX

PS Claim 20; SEQ ID NO 246; 101pp; English.

XX
CC The present invention describes a recombinant fusion protein (I) for
CC detecting binding of a molecule of interest. (I) comprises: (a) a
CC detection domain; (b) a first localisation domain; and (c) a binding
CC domain for the molecule of interest. The detection domain, the first
CC localisation domain and the binding domain for the molecule of interest
CC constituting the recombinant fusion protein for detecting binding of a
CC molecule of interest are operably linked. The binding domain for the
CC molecule of interest is separated from the first localisation domain by 0
CC -20 amino acid residues. The first localisation domain and the binding
CC domain for the molecule of interest both do not occur in a single non-
CC recombinant protein with the same spacing as in the recombinant fusion
CC protein for detecting binding of a molecule of interest. Also described:
CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;
CC (2) a recombinant expression vector comprising the nucleic acid control
CC sequences operably linked to the recombinant nucleic acid molecule; (3) a
CC genetically engineered host cell transfected with the recombinant
CC expression vector; (4) a kit for detecting binding of the molecule of
CC interest; and (5) a method for identifying compounds that alter the
CC binding of the molecule of interest. The recombinant fusion protein is
CC useful for detecting binding of a molecule of interest. The recombinant
CC fusion protein eliminates the need to construct two or more chimeric
CC proteins and enables the monitoring of biochemical events in live, intact
CC or fixed cells. The present sequence is used in the exemplification of
CC the present invention.
XX
SQ Sequence 11 AA;

Query Match 36.4%; Score 4; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRKG 6
| | | |
Db 4 SRKG 7

RESULT 15
AAP50987
ID AAP50987 standard; peptide; 11 AA.
XX
AC AAP50987;
XX
DT 25-MAR-2003 (revised)
DT 08-MAR-1992 (first entry)
XX
DE FTS-derived peptide.
XX
KW Serum thymus factor; FTS.
XX
OS Synthetic.
XX
PN JP60089499-A.
XX
PD 20-MAY-1985.
XX
PF 21-OCT-1983; 83JP-00196079.

XX
PR 21-OCT-1983; 83JP-00196079.
XX
PA (MITH) MITSUI PHARM INC.
XX
DR WPI; 1985-156917/26.
XX
PT New peptide for use in analysis - derived from lysine, tyrosine, glycine,
PT alanine, serine and asparagine units.
XX
PS Claim 1; Page 1; 12pp; Japanese.
XX
CC The peptide is derived from FTS (Pyr-Ala-Lys-Ser-Gln-Gly-Gly-Ser-Asn). It
CC has similar activity to FTS and can be easily labelled with radioactive
CC iodide for use in RIA. See also AAP50412 and AAP50413. (Updated on 25-MAR
CC -2003 to correct PR field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
 | | |
Db 4 AKS 6

RESULT 16

AAP50941

ID AAP50941 standard; peptide; 11 AA.

XX

AC AAP50941;

XX

DT 25-MAR-2003 (revised)

DT 06-OCT-1991 (first entry)

XX

DE Hepatitis B virus (HBV) envelope protein pre-S gene peptide fragment.

XX

KW Immunogen; vaccine; antigen; epitope; diagnosis.

XX

OS Hepatitis B virus.

XX

PN EP154902-A.

XX

PD 18-SEP-1985.

XX

PF 28-FEB-1985; 85EP-00102250.

XX

PR 07-MAR-1984; 84US-00587090.

PR 05-FEB-1985; 85US-00698499.

PR 28-APR-1986; 86US-00856522.

XX

PA (CALY) CALIFORNIA INST OF TECHN.

PA (NYBL-) NEW YORK BLOOD CENTER INC.

XX

PI Neurath AR, Kent SBH;

XX
 DR WPI; 1985-237979/39.
 XX
 PT Pre-s gene coded hepatitis B immunogens - useful in in vaccines for
 PT protection and as diagnostics for detection of antigens and antigens.
 XX
 PS Claim 30; Page 101; 140pp; English.
 XX
 CC The peptides of the invention are immunogens which, esp. when linked to
 CC carriers, may be used in vaccines for conferring protection against HBV,
 CC and in the diagnosis of viral conditions in man and animals and in the
 CC detection of the antigens and antibodies. More specifically, the chain of
 CC AAs is between sequence posn. pre-S 120-174. (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RKG 6
 |||
 Db 9 RKG 11

RESULT 17

AAP82901

ID AAP82901 standard; protein; 11 AA.

XX

AC AAP82901;

XX

DT 25-MAR-2003 (revised)

DT 10-MAR-2003 (revised)

DT 17-DEC-2001 (revised)

DT 23-NOV-1990 (first entry)

XX

DE Activated metalloproteinase CNBr cleavage product #2.

XX

KW metalloproteinase marker; basement membrane type IV collagen;

KW cancer metastases.

XX

OS Homo sapiens.

XX

PN USN7196242-N.

XX

PD 01-NOV-1988.

XX

PF 20-MAY-1988; 88US-00196242.

XX

PR 20-MAY-1988; 88US-00196242.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICE.

XX

PI Liotta LA, Stetlerste W, Kruttsch HC;

XX

DR WPI; 1988-360971/50.

XX
PT Metallo:proteinase marker for cancer metastases - which cleaves basement
PT membrane type IV collagen but does not cleave types I, II or III
PT collagen.
XX
PS Disclosure; Page ?; 31pp; English.
XX
CC Recipient cells (e.g. rat embryo cell lines) transfected with the ras
CC oncogene secrete a metalloproteinase of mol wt 60-75kD. This enzyme
CC cleaves the pepsin resistant domain of basement membrane type IV collagen
CC but does not cleave native types I, II or III. This sequence is a
CC cyanogen bromide cleavage product of the activated form of the enzyme.
CC Metastatic cancer cells can be identified by the level of secretion of
CC the metalloproteinase. Affinity purified antibodies which recognise the N
CC -terminal 30 amino acid residues can distinguish the latent from the
CC activated proteinase. See also AAP82899-P82900 and AAP82902-P82903.
CC (Note: Revised entry submitted to correct the patent number format of US
CC Government-owned NTIS applications to prevent clashes with ongoing US
CC granted patent numbers. For further information please visit the Derwent
CC web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 10-
CC MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GNS 8
|||
Db 6 GNS 8

RESULT 18

AAP80854

ID AAP80854 standard; protein; 11 AA.

XX

AC AAP80854;

XX

DT 15-JAN-1991 (first entry)

XX

DE Sequence of N-terminal methionyl-porcine growth hormone encoded on

DE plasmid pGHX.1.

XX

KW Transgenic animal; somatotrophin.

XX

OS Sus scrofa.

XX

PN WO8808026-A.

XX

PD 20-OCT-1988.

XX

PF 14-APR-1988; 88WO-AU000109.

XX

PR 14-APR-1987; 87AU-00001427.

PR 17-APR-1987; 88AU-00017004.

PR 10-NOV-1987; 87AU-00005326.
 XX
 PA (LUMI-) LUMINIS PTY LTD.
 XX
 PI Seamark RF, Wells JR;
 XX
 DR WPI; 1988-307564/43.
 DR N-PSDB; AAN80882, AAN80885, AAN80886, AAN80887, AAN80888.
 XX
 PT Creating new breed(s) of animals - by introducing a gene sample of a
 PT hormone homologous with the ovum into the male nucleus of a fertilised
 PT ovum.
 XX
 PS Example; Fig 6; 35pp; English.
 XX
 CC A method for creating new breeds of animals comprises (a) obtaining a
 CC recently fertilised ovum, (b) isolating a gene sample of a characterising
 CC hormone homologous with the ovum, (c) introducing the gene sample into
 CC the male nucleus of the ovum prior to fusion with the female nucleus to
 CC form a single cell embryo and (d) subsequently implanting the ovum into a
 CC suitably prepd. female animal. Also claimed is a plasmid expression
 CC vector comprising a plasmid cloning vector including a first cloned
 CC sequence of DNA encoding a non-porcine promoter region and a second
 CC cloned sequence encoding porcine growth hormone activity
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 8 SSL 10

RESULT 19

AAP81302

ID AAP81302 standard; protein; 11 AA.

XX

AC AAP81302;

XX

DT 10-MAR-2003 (revised)

DT 23-NOV-1990 (first entry)

XX

DE Atrial natriuretic polypeptide binding polypeptide T51.

XX

KW Diuretic; atrium cardis; atrial natriuretic peptide binding; T51;
 KW hypotensive action.

XX

OS Mammalia.

XX

PN JP63079598-A.

XX

PD 09-APR-1988.

XX

PF 22-SEP-1986; 86JP-00222192.

XX
 PR 22-SEP-1986; 86JP-00222192.
 XX
 PA (SUNR) SUNTORY LTD.
 XX
 DR WPI; 1988-137132/20.
 XX
 PT Novel polypeptide, with diuretic action - is obtd. from atrium cardis of
 PT mammals showing specific bond to atrial natriuretic polypeptide and gene
 PT coding it.
 XX
 PS Claim 1; Page 2; 23pp; Japanese.
 XX
 CC Peptide binds to atrial natriuretic polypeptide (ANP) and has diuretic
 CC (partic. natriuretic) and hypotensive action. See also AAN81690-93 and
 CC AAP81282-P81309. (Updated on 10-MAR-2003 to add missing OS field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 7 SSL 9

RESULT 20

AAAY07371

ID AAY07371 standard; peptide; 11 AA.

XX

AC AAY07371;

XX

DT 25-MAR-2003 (revised)

DT 16-JUL-1999 (first entry)

XX

DE Matrix metalloprotease antigenic peptide #8.

XX

KW Matrix metalloprotease; inhibitor; tissue damage; angiogenesis; antibody;

KW arthritis; tumour growth; granulomatous inflammatory condition; enzyme;

KW metastasis; sarcoidosis; antigen.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9010228-A.

XX

PD 07-SEP-1990.

XX

PF 01-MAR-1989; 89US-00317407.

XX

PR 01-MAR-1989; 89US-00317407.

PR 26-FEB-1990; 90US-00488460.

XX

PA (USDC) US SEC OF COMMERCE.

PA (USSH) NAT INST OF HEALTH.

XX
 PI Liotta LA, Stetlerste W, Krutzsh H;
 XX
 DR WPI; 1990-290458/38.
 XX
 PT Matrix metallo:proteinase peptide(s) - used to inhibit enzyme in treating
 PT tissue damage caused by activated enzyme.
 XX
 PS Example 3; Page 34; 6lpp; English.
 XX
 CC This sequence represents an antigenic peptide derived from a human type
 CC IV matrix metalloprotease (MMP) protein. The invention relates to MMP
 CC inhibitor peptides which can be used to treat tissue damage caused by
 CC activated MMPs, e.g. for treating inappropriate angiogenesis, arthritis,
 CC tumour growth, invasion and metastasis and granulomatous inflammatory
 CC conditions such as sarcoidosis. Also antibodies to the peptides can be
 CC used to detect the MMPs and can distinguish activated from latent enzyme.
 CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
 CC correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GNS 8
 |||
 Db 6 GNS 8

RESULT 21

AAR07165

ID AAR07165 standard; protein; 11 AA.

XX

AC AAR07165;

XX

DT 24-JAN-1991 (first entry)

XX

DE Synthetic Nerve growth factor (NGF) peptide fragment.

XX

KW Nervous disorders; Alzheimer's disease; Parkinson's disease; stroke.

XX

OS Synthetic.

XX

PN WO9010644-A.

XX

PD 20-SEP-1990.

XX

PF 14-MAR-1989; 89SE-00000899.

XX

PR 14-MAR-1989; 89SE-00000899.

XX

PA (LOPE-) LOPE MED AB.

XX

PI Olson L, Persson H, Ebendal T;

XX

DR WPI; 1990-304983/40.
 XX
 PT New peptide fragments of nerve growth factor or its precursor - used to
 PT raise specific antibodies for immunoassay, esp. for brain tissue.
 XX
 PS Disclosure; Page 11; 24pp; English.
 XX
 CC Peptides are Abs raised to them are useful in detecting the presence of
 CC NGF and precursors, allowing early diagnosis and treatment of nervous
 CC disorders eg. Alzheimer's and Parkinson's disease, spinal cord injury,
 CC stroke etc. Peptide corresponds to AAs 111 to 120 of rat NGF
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
 |||
 Db 4 SRK 6

RESULT 22

AAR10045

ID AAR10045 standard; protein; 11 AA.

XX

AC AAR10045;

XX

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 09-JAN-2003 (revised)

DT 14-MAR-1991 (first entry)

XX

DE N-terminal fusion of VP2 to hexapeptide.

XX

KW VP2 protein; infectious bursal disease virus; poultry vaccine.

XX

OS Infectious bursal disease virus.

XX

FH Key Location/Qualifiers

FT Peptide 7. .11

FT /label= VP2 peptide

XX

PN WO9015140-A.

XX

PD 13-DEC-1990.

XX

PF 30-MAY-1989; 89AU-00004469.

XX

PR 30-MAY-1989; 89AU-00004469.

XX

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

XX

PI Azad AA, Macreadie JG, Mckern NM, Vaughan PR, Jagadish MN;

PI Fahey KJ, Chapman JJ, Heine HG;

XX

DR WPI; 1991-007210/01.
 DR N-PSDB; AAQ10155.
 XX
 PT Highly immunogenic VP2 protein - of infectious bursal disease virus,
 PT useful in vaccine compsn. for immunisation against the disease in
 PT poultry.
 XX
 PS Disclosure; Page 31; 70pp; English.
 XX
 CC This sequence comprises the region encompassing the N-terminal fusion of
 CC a vector (pIP201) hexapeptide prod. and the N-terminal Met and residues -
 CC 1(Thr) - 5(Asp) of the VP2 protein. The resultant prod. constitutes a
 CC highly immunogenic form of VP2. A hybrid VP2 can also be constructed,
 CC having an N-terminal from one strain of IBDV and a C- terminal from
 CC another strain of IBDV. The proteins can be used in vaccines against IBDV
 CC disease in poultry. See also AAQ10373. (Updated on 09-JAN-2003 to add
 CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated
 CC on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct
 CC OS field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
 |||
 Db 2 NSS 4

RESULT 23

AAR14094

ID AAR14094 standard; protein; 11 AA.

XX

AC AAR14094;

XX

DT 25-MAR-2003 (revised)

DT 04-DEC-1991 (first entry)

XX

DE Pre-S(1-11) immunogenic peptide based on HBV subtype adw2.

XX

KW hepatitis B virus; vaccine; liposome-peptide complex.

XX

OS Synthetic.

XX

PN EP448126-A.

XX

PD 25-SEP-1991.

XX

PF 28-FEB-1985; 91EP-00105948.

XX

PR 07-MAR-1984; 84US-00587090.

PR 05-FEB-1985; 85US-00698499.

XX

PA (NYBL-) NEW YORK BLOOD CENTER INC.

PA (CALY) CALIFORNIA INST OF TECHN.

XX
 PI Neurath AR, Kent SBH;
 XX
 DR WPI; 1991-283144/39.
 XX
 PT Synthetic lipid vesicle carrier linked to pre-S gene coded peptide - the
 PT peptide is a hepatitis B immunogen, vaccine or diagnostic.
 XX
 PS Disclosure; Page 13; 54pp; English.
 XX
 CC This peptide is one of ten preferred HBV antigenic sequences which are
 CC suitable for attachment to lipid vesicles for use as vaccines. The lipid
 CC vesicle carrier is stabilised by cross-linking and has covalently bonded
 CC sites on its outer surface to bind the peptide. See AAR14086-R14095.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
 CC correct PA field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RKG 6
 |||
 Db 9 RKG 11

RESULT 24

AAR44308

ID AAR44308 standard; protein; 11 AA.

XX

AC AAR44308;

XX

DT 20-DEC-1993 (first entry)

XX

DE Ballast constituent in pINT90d pro-insulin fusion protein.

XX

KW Fusion protein; ballast constituent; monkey pro-insulin; increased;

KW recombinant protein production; HMG CoA reductase;

KW human 3-hydroxy-3-methylglutaryl-coenzyme A-reductase.

XX

OS Synthetic.

XX

PN US5227293-A.

XX

PD 13-JUL-1993.

XX

PF 23-APR-1992; 92US-00838221.

XX

PR 29-AUG-1989; 89US-00399874.

PR 28-AUG-1990; 90WO-US004840.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (FARH) HOECHST AG.

XX

PI Stengelin S, Ulmer W, Habermann P, Uhlmann E, Seed B;

XX
 DR WPI; 1991-102070/14.
 DR N-PSDB; AAQ51807.
 XX
 PT Prepn. of fusion proteins contg. ballast constituent and protein - giving
 PT prods. which are protease resistant or insoluble.
 XX
 PS Example 17; Col 7-8; 22pp; English.
 XX
 CC Sequence AAR44308 is an example of a specific ballast constituent peptide
 CC which corresponds to a preferred generic coding sequence. The invention
 CC covers fusion proteins in which a short ballast constituent is fused to a
 CC desired protein, esp. to modified pro- insulin, to increase recombinant
 CC production of the protein. See AAR44301-R44312
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GNS 8
 |||
 Db 7 GNS 9

RESULT 25

AAR31358

ID AAR31358 standard; peptide; 11 AA.

XX

AC AAR31358;

XX

DT 25-MAR-2003 (revised)

DT 20-MAY-1998 (first entry)

XX

DE Antimicrobial peptide #12 derived from bovine lactoferrin.

XX

KW antimicrobial agent; iron-binding protein; athlete's foot; mastitis;

KW antibacterial agent.

XX

OS Synthetic.

XX

PN EP503939-A1.

XX

PD 16-SEP-1992.

XX

PF 12-MAR-1992; 92EP-00302125.

XX

PR 13-MAR-1991; 91JP-00048196.

PR 24-APR-1991; 91JP-00094492.

PR 24-APR-1991; 91JP-00094493.

XX

PA (MORG) MORINAGA MILK IND CO LTD.

XX

PI Tomita M, Kawase K, Takase M, Bellamy WR, Yamauchi K;

PI Wakabayashi H, Tokita Y;

XX

DR WPI; 1992-310006/38.
 XX
 PT New antimicrobial peptide(s) - active against e.g. *Listeria*
 PT *monocytogenes*, *Staphylococcus aureus*, *Pseudomonas aeruginosa* and
 PT *Klebsiella pneumoniae*, for treating e.g. diarrhoea, mastitis, etc.
 XX
 PS Claim 8; Page 17; 19pp; English.
 XX
 CC This synthetic peptide has a sequence derived from bovine lactoferrin.
 CC The peptide has stronger antimicrobial activity than unhydrolysed
 CC lactoferrin and improved heat resistance. The peptide had a minimum
 CC inhibitory concentration (microM) of 1.5, 3, 6 and 25 against *Listeria*
 CC *monocytogenes*, *Staphylococcus aureus*, *Pseudomonas aeruginosa* and
 CC *Klebsiella pneumoniae*, respectively. This and other peptides derived from
 CC hydrolysed lactoferrin can be incorporated into foods, human or
 CC veterinary compositions (e.g. for treating mastitis and athlete's foot),
 CC toiletries, cosmetics, cleaning agents, etc. See AAR31350-R31361.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KSR 4
 |||
 Db 1 KSR 3

RESULT 26

AAR24850

ID AAR24850 standard; protein; 11 AA.

XX

AC AAR24850;

XX

DT 25-MAR-2003 (revised)

DT 08-DEC-1992 (first entry)

XX

DE Weight regulating peptide 33.

XX

KW Amphetamine; appetite suppressor.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 2

FT /label= GLY, ALA, VAL, LEU, SER, THR, CYS, MET, ASP, GLU,

FT ASN, GLN, LYS, HIS, ARG, PHE, TYR, TRP, PRO, OTHER

FT /note= "cystine, hydroxylysine, hydroxyproline"

FT Misc-difference 3

FT /label= GLY, ALA, VAL, LEU, SER, THR, CYS, MET, ASP, GLU,

FT ASN, GLN, LYS, HIS, ARG, PHE, TYR, TRP, PRO, OTHER

FT /note= "cystine, hydroxylysine, hydroxyproline"

XX

PN WO9209296-A1.

XX

PD 11-JUN-1992.
 XX
 PF 20-NOV-1991; 91WO-US008497.
 XX
 PR 21-NOV-1990; 90US-00616910.
 XX
 PA (GEOU) UNIV GEORGETOWN.
 XX
 PI Fleming PJ, Kent UM;
 XX
 DR WPI; 1992-216791/26.
 XX
 PT New dodeca:peptide cpds. - used for regulating wt. gain in mammals or for
 PT producing antibodies for attenuating such effects.
 XX
 PS Disclosure; Page 10; 34pp; English.
 XX
 CC The sequences given in AAR24818-61 are new peptides which comprise at
 CC least 6 amino acids from the sequence given in AAR24814. The remaining
 CC amino acids are each Gly, Ala, Val, Leu, Ser, Thr, Cys, cystine, Met,
 CC Asp, Glu, Asn, Gln, Lys, hydroxylysine, His, Arg, Phe, Tyr, Trp, Pro or
 CC hydroxyproline. These peptides used for the regulation of weight gain in
 CC mammals and can be used instead of amphetamine, which is largely used as
 CC an appetite suppressor. These peptides can also be used to prepare
 CC antibodies. Such antibodies can be used to attenuate the effect of the
 CC peptides in a host or to detect, quantify or purify the peptides.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RKG 6
 |||
 Db 4 RKG 6

RESULT 27

AAR28088

ID AAR28088 standard; protein; 11 AA.

XX

AC AAR28088;

XX

DT 25-MAR-2003 (revised)

DT 27-NOV-1992 (first entry)

XX

DE Cell-to-cell binding inhibiting peptide subunit (13).

XX

KW Adhesion; integrin; multimer.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Cross-links 6. .11

FT /note= "sequence linked by interchain amide bond at Lys

FT position to Glu residue on Arg5-Glu-Ser-Arg-Gly-Asp-Val
FT sequence (see AAR28087)"

XX

PN WO9208476-A1.

XX

PD 29-MAY-1992.

XX

PF 07-NOV-1991; 91WO-US008328.

XX

PR 07-NOV-1990; 90US-00610363.

XX

PA (SCRI) SCRIPPS RES INST.

XX

PI Ruggeri ZM, Houghten RA;

XX

DR WPI; 1992-199940/24.

XX

PT Peptides inhibiting binding of adhesion mols. to cells expressing
PT integrins - for treating and preventing thrombus formation and diseases
PT associated with platelet aggregation.

XX

PS Disclosure; Page 37-38; 70pp; English.

XX

CC A peptide which inhibits binding of adhesion mols. to cells expressing
CC integrins comprises two subunits having the sequences given in AAR28087-
CC 88, held together by an interchain stable bond. The sequence RGD is in
CC each of the subunits. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KSR 4

|||

Db 6 KSR 8

RESULT 28

AAR25763

ID AAR25763 standard; protein; 11 AA.

XX

AC AAR25763;

XX

DT 25-MAR-2003 (revised)

DT 15-JAN-1993 (first entry)

XX

DE Histone H2B peptide - N-Ac-[Lupus 2'(2-12)]-CONH2.

XX

KW Autoimmune; systemic lupus erythematosus; SLE; antibody; domain.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal is acetylated"

FT Modified-site 11
 FT /note= "C-terminal is amidated"
 XX
 PN WO9211029-A1.
 XX
 PD 09-JUL-1992.
 XX
 PF 17-DEC-1991; 91WO-US009176.
 XX
 PR 17-DEC-1990; 90US-00628858.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Dintzis HM, Dintzis RZ, Blodgett JK, Cheronis JC;
 PI Kirschenheuter G;
 XX
 DR WPI; 1992-249851/30.
 XX
 PT Suppression of undesired immune responses using an antigenic construct -
 PT for treating pollen allergies and auto:immune diseases e.g. multiple
 PT sclerosis, Myasthenia Gravis.
 XX
 PS Example 3; Page 71; 230pp; English.
 XX
 CC In order to suppress the autoimmune response to histone H2B that occurs
 CC in the (NZBxNZW) F, murine model of systemic lupus erythematosus (SLE),
 CC the antibody binding domain(s) of histone H2B had to be identified. It is
 CC known that removal of the H2B N-terminal region with trypsin results in a
 CC loss of antigenicity (Portanova, J.P., et al., J. Immunol. 38, 446-457,
 CC (1987)). Attention was therefore, focussed on the synthesis of peptides
 CC derived from this region of histone H2B. The peptides synthesised
 CC together with their respective designations are represented in AAR25751-
 CC 65. The antigen recognised by (NZBxNZW) F, mice was assigned as being
 CC within H2B residues 3-12. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3

|||

Db 3 AKS 5

RESULT 29

AAR27520

ID AAR27520 standard; peptide; 11 AA.

XX

AC AAR27520;

XX

DT 25-MAR-2003 (revised)

DT 10-MAR-1993 (first entry)

XX

DE Effector cell protease receptor-1 derived peptide.

XX

KW EPR-1; antibodies; chronic lymphocytic leukaemia; hairy cell leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO9216558-A1.
 XX
 PD 01-OCT-1992.
 XX
 PF 12-MAR-1992; 92WO-US002109.
 XX
 PR 12-MAR-1991; 91US-00667957.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Altieri DC, Edgington TS;
 XX
 DR WPI; 1992-349160/42.
 XX
 PT Cell surface receptors homologous to coagulation factors V and VIII - for
 PT monitoring the response to treatment of chronic lymphocytic leukaemia.
 XX
 PS Claim 1; Page 71; 83pp; English.
 XX
 CC The peptide is derived from effector cell protease receptor-1 (EPR-1)
 CC Antibodies raised against it can be used for monitoring treatment of
 CC patients afflicted with chronic lymphocytic leukaemia, hairy cell
 CC leukaemia and other diseases in which expression of receptors homologous
 CC to coagulation factors V and VIII is correlated with the disease state.
 CC The antibodies can also be used for detecting EPR-1 cell surface
 CC receptors. See also AAR27515-R27521. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GNS 8
 |||
 Db 1 GNS 3

RESULT-30

AAR26085

ID AAR26085 standard; peptide; 11 AA.

XX

AC AAR26085;

XX

DT 25-MAR-2003 (revised)

DT 01-FEB-1993 (first entry)

XX

DE Immunising peptide fragment #5 of T cell receptor.

XX

KW TCR; beta chain; rheumatoid arthritis; multiple sclerosis;

KW autoimmune disease; diabetes; T-cell lymphoma; vaccination; immunisation.

XX

OS Synthetic.
 XX
 PN WO9212996-A2.
 XX
 PD 06-AUG-1992.
 XX
 PF 21-JAN-1992; 92WO-US000482.
 XX
 PR 22-JAN-1991; 91US-00644611.
 XX
 PA (IMMU-) IMMUNE RESPONSE CORP.
 XX
 PI Howell MD, Brostoff SW, Carlo DJ;
 XX
 DR WPI; 1992-284600/34.
 XX
 PT Treatment of auto:immune diseases e.g. rheumatoid arthritis - using
 PT vaccine contg. T-cell receptors from surface of T-cells which mediate the
 PT diseases.
 XX
 PS Disclosure; Page 15; 87pp; English.
 XX
 CC This peptide fragment of the T-cell receptor is used as an immunising
 CC peptide as part of a vaccine used to control rheumatoid arthritis or
 CC multiple sclerosis, but can also be used against other autoimmune
 CC diseases (eg. diabetes) or T-cell lymphoma. The sequence is part of a
 CC beta chain VDJ region. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 2 SSL 4

RESULT 31

AAR26084

ID AAR26084 standard; peptide; 11 AA.

XX

AC AAR26084;

XX

DT 25-MAR-2003 (revised)

DT 01-FEB-1993 (first entry)

XX

DE Immunising peptide fragment #4 of T cell receptor.

XX

KW TCR; beta chain; rheumatoid arthritis; multiple sclerosis;

KW autoimmune disease; diabetes; T-cell lymphoma; vaccination; immunisation.

XX

OS Synthetic.

XX

PN WO9212996-A2.

XX

PD 06-AUG-1992.
 XX
 PF 21-JAN-1992; 92WO-US000482.
 XX
 PR 22-JAN-1991; 91US-00644611.
 XX
 PA (IMMU-) IMMUNE RESPONSE CORP.
 XX
 PI Howell MD, Brostoff SW, Carlo DJ;
 XX
 DR WPI; 1992-284600/34.
 XX
 PT Treatment of auto:immune diseases e.g. rheumatoid arthritis - using
 PT vaccine contg. T-cell receptors from surface of T-cells which mediate the
 PT diseases.
 XX
 PS Disclosure; Page 15; 87pp; English.
 XX
 CC This peptide fragment of the T-cell receptor is used as an immunising
 CC peptide as part of a vaccine used to control rheumatoid arthritis or
 CC multiple sclerosis, but can also be used against other autoimmune
 CC diseases (eg. diabetes) or T-cell lymphoma. The sequence is part of a
 CC beta chain VDJ region. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 2 SSL 4

RESULT 32

AAR26832

ID AAR26832 standard; peptide; 11 AA.

XX

AC AAR26832;

XX

DT 20-MAY-1998 (first entry)

XX

DE ~~TY-11(6)-FGF-analogue.~~

XX

KW Fibroblast growth factor; DMSO oxidation; disulphide peptides;
 KW oxidative folding; dimethyl sulphoxide.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT disulfide_bond 2. .7

FT /note= "bridge formed by DMSO oxidation"

XX

PN US5144006-A.

XX

PD 01-SEP-1992.

XX
 PF 13-JUN-1991; 91US-00714659.
 XX
 PR 13-JUN-1991; 91US-00714659.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Tam JP;
 XX
 DR WPI; 1992-315567/38.
 XX
 PT Oxidative folding of peptide and protein substrates - using hydrocarbon
 PT sulphoxide(s), e.g. DMSO, with wide pH and temp. range, for synthesis of
 PT e.g. endothelin.
 XX
 PS Disclosure; Fig 1; 14pp; English.
 XX
 CC This peptide is one of a series of basic peptides derived from the
 CC receptor-recognition site comprised of residues 100-115 of human basic
 CC fibroblast growth factor. This highly basic and hydrophobic sequence
 CC contained no cysteine but was converted to cysteinyl- containing
 CC sequences so that the peptides could be used as models to show the
 CC effectiveness of DMSO as an oxidising agent in the novel method. Using
 CC 20% DMSO in aq.soln. as the oxidative folding reagent, the disulphide
 CC formation by DMSO oxidation was rapid in all the model peptides. The
 CC optimal pH range for disulphide formation is 3-8, although this can be
 CC extended to 2-10 with some substrates. The method can be used in the
 CC synthesis of defensins (anti-microbials), endothelin and its precursor
 CC big endothelin. See also AAR26833-R26840
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
 |||
 Db 4 SRK 6

RESULT 33

AAR26834

ID AAR26834-standard; peptide; 11-AA.

XX

AC AAR26834;

XX

DT 20-MAY-1998 (first entry)

XX

DE CY-11(8) FGF analogue.

XX

KW Fibroblast growth factor; DMSO oxidation; disulphide peptides;

KW oxidative folding; dimethyl sulphoxide.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT disulfide_bond 1. .8
 FT /note= "bridge formed by DMSO oxidation"
 XX
 PN US5144006-A.
 XX
 PD 01-SEP-1992.
 XX
 PF 13-JUN-1991; 91US-00714659.
 XX
 PR 13-JUN-1991; 91US-00714659.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Tam JP;
 XX
 DR WPI; 1992-315567/38.
 XX
 PT Oxidative folding of peptide and protein substrates - using hydrocarbon
 PT sulphoxide(s), e.g. DMSO, with wide pH and temp. range, for synthesis of
 PT e.g. endothelin.
 XX
 PS Disclosure; Fig 1; 14pp; English.
 XX
 CC This peptide is one of a series of basic peptides derived from the
 CC receptor-recognition site comprised of residues 100-115 of human basic
 CC fibroblast growth factor. This highly basic and hydrophobic sequence
 CC contained no cysteine but was converted to cysteinyl- containing
 CC sequences so that the peptides could be used as models to show the
 CC effectiveness of DMSO as an oxidising agent in the novel method. Using
 CC 20% DMSO in aq.soln. as the oxidative folding reagent, the disulphide
 CC formation by DMSO oxidation was rapid in all the model peptides. The
 CC optimal pH range for disulphide formation is 3-8, although this can be
 CC extended to 2-10 with some substrates. The method can be used in the
 CC synthesis of defensins (anti-microbials), endothelin and its precursor
 CC big endothelin. See AAR26832-R26840
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5

|||

Db 4 SRK 6

RESULT 34

AAR26833

ID AAR26833 standard; peptide; 11 AA.

XX

AC AAR26833;

XX

DT 20-MAY-1998 (first entry)

XX

DE CY-11(7) FGF analogue.

XX

KW Fibroblast growth factor; DMSO oxidation; disulphide peptides;
 KW oxidative folding; dimethyl sulphoxide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT disulfide_bond 1. .7
 FT /note= "bridge formed by DMSO oxidation"
 XX
 PN US5144006-A.
 XX
 PD 01-SEP-1992.
 XX
 PF 13-JUN-1991; 91US-00714659.
 XX
 PR 13-JUN-1991; 91US-00714659.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Tam JP;
 XX
 DR WPI; 1992-315567/38.
 XX
 PT Oxidative folding of peptide and protein substrates - using hydrocarbon
 PT sulphoxide(s), e.g. DMSO, with wide pH and temp. range, for synthesis of
 PT e.g. endothelin.
 XX
 PS Disclosure; Fig 1; 14pp; English.
 XX
 CC This peptide is one of a series of basic peptides derived from the
 CC receptor-recognition site comprised of residues 100-115 of human basic
 CC fibroblast growth factor. This highly basic and hydrophobic sequence
 CC contained no cysteine but was converted to cysteinyl- containing
 CC sequences so that the peptides could be used as models to show the
 CC effectiveness of DMSO as an oxidising agent in the novel method. Using
 CC 20% DMSO in aq.soln. as the oxidative folding reagent, the disulphide
 CC formation by DMSO oxidation was rapid in all the model peptides. The
 CC optimal pH range for disulphide formation is 3-8, although this can be
 CC extended to 2-10 with some substrates. The method can be used in the
 CC synthesis of defensins (anti-microbials), endothelin and its precursor
 CC big endothelin. See also AAR26833-R26840
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
 |||
 Db 4 SRK 6

RESULT 35
 AAR26835
 ID AAR26835 standard; peptide; 11 AA.
 XX

AC AAR26835;
 XX
 DT 20-MAY-1998 (first entry)
 XX
 DE CY-11(9) FGF analogue.
 XX
 KW Fibroblast growth factor; DMSO oxidation; disulphide peptides;
 KW oxidative folding; dimethyl sulphoxide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT disulfide_bond 1. .9
 FT /note= "bridge formed by DMSO oxidation"
 XX
 PN US5144006-A.
 XX
 PD 01-SEP-1992.
 XX
 PF 13-JUN-1991; 91US-00714659.
 XX
 PR 13-JUN-1991; 91US-00714659.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 XX
 PI Tam JP;
 XX
 DR WPI; 1992-315567/38.
 XX
 PT Oxidative folding of peptide and protein substrates - using hydrocarbon
 PT sulphoxide(s), e.g. DMSO, with wide pH and temp. range, for synthesis of
 PT e.g. endothelin.
 XX
 PS Disclosure; Fig 1; 14pp; English.
 XX
 CC This peptide is one of a series of basic peptides derived from the
 CC receptor-recognition site comprised of residues 100-115 of human basic
 CC fibroblast growth factor. This highly basic and hydrophobic sequence
 CC contained no cysteine but was converted to cysteinyl- containing
 CC sequences so that the peptides could be used as models to show the
 CC effectiveness of DMSO as an oxidising agent in the novel method. Using
 CC 20% DMSO in aq.soln. as the oxidative folding reagent, the disulphide
 CC formation by DMSO oxidation was rapid in all the model peptides. The
 CC optimal pH-range for disulphide formation is 3-8, although this can be
 CC extended to 2-10 with some substrates. The method can be used in the
 CC synthesis of defensins (anti-microbials), endothelin and its precursor
 CC big endothelin. See AAR26832-R26840
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
 |||
 Db 4 SRK 6

RESULT 36

AAR36904

ID AAR36904 standard; peptide; 11 AA.

XX

AC AAR36904;

XX

DT 25-MAR-2003 (revised)

DT 02-SEP-1993 (first entry)

XX

DE Insulin-like growth factor-II functional derivative.

XX

KW IGF-II; disorder; treatment; survival; retinal neuronal cells; promotion;

KW injury; ageing; disease; photodegeneration; trauma; axotomy;

KW neurotoxic-excitatory degeneration; diabetic retinopathy;

KW ischemic neuronal degeneration; inherited retinal dystrophy;

KW Alzheimer's disease; infantile malignant osteopetrosis; cholestasis;

KW ceroid-lipofuscosis; cyclic.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1. .11

XX

PN WO9308826-A1.

XX

PD 13-MAY-1993.

XX

PF 03-NOV-1992; 92WO-US009443.

XX

PR 08-NOV-1991; 91US-00790690.

PR 15-OCT-1992; 92US-00963329.

XX

PA (CEPH-) CEPHALON INC.

XX

PI Bozyczko-Coyne D, Neff N, Lewis ME, Iqbal M;

XX

DR WPI; 1993-167389/20.

XX

PT Use of IGF-I or IGF-II or their functional derivs. - for treating

PT disorders characterised by death and/or dysfunction of retinal cells.

XX

PS ~~Example; Page 69; 97pp; English.~~

XX

CC The sequence is that of a functional derivative of human insulin-like
 CC growth factor (IGF)-II which promotes the survival of retinal neuronal
 CC cells. It can be used for the treatment of retinal neuronal tissues which
 CC are suffering from the effects of injury, ageing and/or disease such as
 CC photodegeneration, trauma, axotomy, neurotoxic-excitatory degeneration,
 CC ischemic neuronal degeneration, inherited retinal dystrophy, diabetic
 CC retinopathy, Alzheimer's disease, infantile malignant osteopetrosis,
 CC ceroid lipofuscosis or cholestasis. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
|||
Db 7 AKS 9

RESULT 37

AAR36924

ID AAR36924 standard; peptide; 11 AA.

XX

AC AAR36924;

XX

DT 25-MAR-2003 (revised)

DT 02-SEP-1993 (first entry)

XX

DE Insulin-like growth factor-II functional derivative.

XX

KW IGF-II; disorder; treatment; survival; retinal neuronal cells; promotion;

KW injury; ageing; disease; photodegeneration; trauma; axotomy;

KW neurotoxic-excitatory degeneration; diabetic retinopathy;

KW ischemic neuronal degeneration; inherited retinal dystrophy;

KW Alzheimer's disease; infantile malignant osteopetrosis; cholestasis;

KW ceroid-lipofuscosis; cyclic.

XX

OS Synthetic.

XX

PN WO9308826-A1.

XX

PD 13-MAY-1993.

XX

PF 03-NOV-1992; 92WO-US009443.

XX

PR 08-NOV-1991; 91US-00790690.

PR 15-OCT-1992; 92US-00963329.

XX

PA (CEPH-) CEPHALON INC.

XX

PI Bozyczko-Coyne D, Neff N, Lewis ME, Iqbal M;

XX

DR WPI; 1993-167389/20.

XX

PT Use of IGF-I or IGF-II or their functional derivs. - for treating
PT disorders characterised by death and/or dysfunction of retinal cells.

XX

PS Example; Page 76; 97pp; English.

XX

CC The sequence is that of a functional derivative of human insulin-like
CC growth factor (IGF)-II which promotes the survival of retinal neuronal
CC cells. It can be used for the treatment of retinal neuronal tissues which
CC are suffering from the effects of injury, ageing and/or disease such as
CC photodegeneration, trauma, axotomy, neurotoxic-excitatory degeneration,
CC ischemic neuronal degeneration, inherited retinal dystrophy, diabetic
CC retinopathy, Alzheimer's disease, infantile malignant osteopetrosis,
CC ceroid lipofuscosis or cholestasis. (Updated on 25-MAR-2003 to correct PN

CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
|||
Db 8 AKS 10

RESULT 38

AAR36905

ID AAR36905 standard; peptide; 11 AA.

XX

AC AAR36905;

XX

DT 25-MAR-2003 (revised)

DT 02-SEP-1993 (first entry)

XX

DE Insulin-like growth factor-II functional derivative.

XX

KW IGF-II; disorder; treatment; survival; retinal neuronal cells; promotion;

KW injury; ageing; disease; photodegeneration; trauma; axotomy;

KW neurotoxic-excitatory degeneration; diabetic retinopathy;

KW ischemic neuronal degeneration; inherited retinal dystrophy;

KW Alzheimer's disease; infantile malignant osteopetrosis; cholestasis;

KW ceroid-lipofuscosis; cyclic.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1. .11

XX

PN WO9308826-A1.

XX

PD 13-MAY-1993.

XX

PF 03-NOV-1992; 92WO-US009443.

XX

PR 08-NOV-1991; 91US-00790690.

PR 15-OCT-1992; 92US-00963329.

XX

PA (CEPH-) CEPHALON INC.

XX

PI Bozyczko-Coyne D, Neff N, Lewis ME, Iqbal M;

XX

DR WPI; 1993-167389/20.

XX

PT Use of IGF-I or IGF-II or their functional derivs. - for treating

PT disorders characterised by death and/or dysfunction of retinal cells.

XX

PS Example; Page 70; 97pp; English.

XX

CC The sequence is that of a functional derivative of human insulin-like

CC growth factor (IGF)-II which promotes the survival of retinal neuronal
 CC cells. It can be used for the treatment of retinal neuronal tissues which
 CC are suffering from the effects of injury, ageing and/or disease such as
 CC photodegeneration, trauma, axotomy, neurotoxic-excitatory degeneration,
 CC ischemic neuronal degeneration, inherited retinal dystrophy, diabetic
 CC retinopathy, Alzheimer's disease, infantile malignant osteopetrosis,
 CC ceroid lipofuscosis or cholestasis. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
 |||
 Db 7 AKS 9

RESULT 39

AAR36894

ID AAR36894 standard; peptide; 11 AA.

XX

AC AAR36894;

XX

DT 25-MAR-2003 (revised)

DT 02-SEP-1993 (first entry)

XX

DE Insulin-like growth factor-II functional derivative.

XX

KW IGF-II; disorder; treatment; survival; retinal neuronal cells; promotion;

KW injury; ageing; disease; photodegeneration; trauma; axotomy;

KW neurotoxic-excitatory degeneration; diabetic retinopathy;

KW ischemic neuronal degeneration; inherited retinal dystrophy;

KW Alzheimer's disease; infantile malignant osteopetrosis; cholestasis;

KW ceroid-lipofuscosis; cyclic.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Disulfide-bond 1. .11

FT Misc-difference 3

FT /note="D-form"

XX

PN WO9308826-A1.

XX

PD 13-MAY-1993.

XX

PF 03-NOV-1992; 92WO-US009443.

XX

PR 08-NOV-1991; 91US-00790690.

PR 15-OCT-1992; 92US-00963329.

XX

PA (CEPH-) CEPHALON INC.

XX

PI Bozyczko-Coyne D, Neff N, Lewis ME, Iqbal M;

XX
 DR WPI; 1993-167389/20.
 XX
 PT Use of IGF-I or IGF-II or their functional derivs. - for treating
 PT disorders characterised by death and/or dysfunction of retinal cells.
 XX
 PS Example; Page 66; 97pp; English.
 XX
 CC The sequence is that of a functional derivative of human insulin-like
 CC growth factor (IGF)-II which promotes the survival of retinal neuronal
 CC cells. It can be used for the treatment of retinal neuronal tissues which
 CC are suffering from the effects of injury, ageing and/or disease such as
 CC photodegeneration, trauma, axotomy, neurotoxic-excitatory degeneration,
 CC ischemic neuronal degeneration, inherited retinal dystrophy, diabetic
 CC retinopathy, Alzheimer's disease, infantile malignant osteopetrosis,
 CC ceroid lipofuscosi s or cholestasis. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
 |||
 Db 7 AKS 9

RESULT 40
 AAR36917
 ID AAR36917 standard; peptide; 11 AA.
 XX
 AC AAR36917;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-SEP-1993 (first entry)
 XX
 DE Insulin-like growth factor-II functional derivative.
 XX
 KW IGF-II; disorder; treatment; survival; retinal neuronal cells; promotion;
 KW injury; ageing; disease; photodegeneration; trauma; axotomy;
 KW neurotoxic-excitatory degeneration; diabetic retinopathy;
 KW ~~ischemic neuronal degeneration; inherited retinal dystrophy;~~
 KW Alzheimer's disease; infantile malignant osteopetrosis; cholestasis;
 KW ceroid-lipofuscosi s; cyclic.
 XX
 OS Synthetic.
 XX
 PN WO9308826-A1.
 XX
 PD 13-MAY-1993.
 XX
 PF 03-NOV-1992; 92WO-US009443.
 XX
 PR 08-NOV-1991; 91US-00790690.
 PR 15-OCT-1992; 92US-00963329.

XX
PA (CEPH-) CEPHALON INC.
XX
PI Bozyczko-Coyne D, Neff N, Lewis ME, Iqbal M;
XX
DR WPI; 1993-167389/20.
XX
PT Use of IGF-I or IGF-II or their functional derivs. - for treating
PT disorders characterised by death and/or dysfunction of retinal cells.
XX
PS Example; Page 74; 97pp; English.
XX
CC The sequence is that of a functional derivative of human insulin-like
CC growth factor (IGF)-II which promotes the survival of retinal neuronal
CC cells. It can be used for the treatment of retinal neuronal tissues which
CC are suffering from the effects of injury, ageing and/or disease such as
CC photodegeneration, trauma, axotomy, neurotoxic-excitatory degeneration,
CC ischemic neuronal degeneration, inherited retinal dystrophy, diabetic
CC retinopathy, Alzheimer's disease, infantile malignant osteopetrosis,
CC ceroid lipofuscososis or cholestasis. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
|||
Db 8 AKS 10

RESULT 41

AAR36874

ID AAR36874 standard; peptide; 11 AA.

XX

AC AAR36874;

XX

DT 25-MAR-2003 (revised)

DT 02-SEP-1993 (first entry)

XX

DE Insulin-like growth factor-I functional derivative.

XX

KW IGF-I; disorder; treatment; survival; retinal neuronal cells; promotion;
KW injury; ageing; disease; photodegeneration; trauma; axotomy;
KW neurotoxic-excitatory degeneration; diabetic retinopathy;
KW ischemic neuronal degeneration; inherited retinal dystrophy;
KW Alzheimer's disease; infantile malignant osteopetrosis; cholestasis;
KW ceroid-lipofuscososis; loop peptide.

XX

OS Homo sapiens.

XX

PN W09308826-A1.

XX

PD 13-MAY-1993.

XX

PF 03-NOV-1992; 92WO-US009443.
 XX
 PR 08-NOV-1991; 91US-00790690.
 PR 15-OCT-1992; 92US-00963329.
 XX
 PA (CEPH-) CEPHALON INC.
 XX
 PI Bozyczko-Coyne D, Neff N, Lewis ME, Iqbal M;
 XX
 DR WPI; 1993-167389/20.
 XX
 PT Use of IGF-I or IGF-II or their functional derivs. - for treating
 PT disorders characterised by death and/or dysfunction of retinal cells.
 XX
 PS Example; Page 60; 97pp; English.
 XX
 CC The sequence is that of a functional derivative of human insulin-like
 CC growth factor (IGF)-I which promotes the survival of retinal neuronal
 CC cells. It can be used for the treatment of retinal neuronal tissues which
 CC are suffering from the effects of injury, ageing and/or disease such as
 CC photodegeneration, trauma, axotomy, neurotoxic-excitatory degeneration,
 CC ischemic neuronal degeneration, inherited retinal dystrophy, diabetic
 CC retinopathy, Alzheimer's disease, infantile malignant osteopetrosis,
 CC ceroid lipofuscosis or cholestasis. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
 |||
 Db 7 AKS 9

RESULT 42

AAR36914

ID AAR36914 standard; peptide; 11 AA.

XX

AC AAR36914;

XX

DT 25-MAR-2003 (revised)

DT 02-SEP-1993 (first entry)

XX

DE Insulin-like growth factor-II functional derivative.

XX

KW IGF-II; disorder; treatment; survival; retinal neuronal cells; promotion;

KW injury; ageing; disease; photodegeneration; trauma; axotomy;

KW neurotoxic-excitatory degeneration; diabetic retinopathy;

KW ischemic neuronal degeneration; inherited retinal dystrophy;

KW Alzheimer's disease; infantile malignant osteopetrosis; cholestasis;

KW ceroid-lipofuscosis; cyclic.

XX

OS Synthetic.

XX

PN WO9308826-A1.
 XX
 PD 13-MAY-1993.
 XX
 PF 03-NOV-1992; 92WO-US009443.
 XX
 PR 08-NOV-1991; 91US-00790690.
 PR 15-OCT-1992; 92US-00963329.
 XX
 PA (CEPH-) CEPHALON INC.
 XX
 PI Bozyczko-Coyne D, Neff N, Lewis ME, Iqbal M;
 XX
 DR WPI; 1993-167389/20.
 XX
 PT Use of IGF-I or IGF-II or their functional derivs. - for treating
 PT disorders characterised by death and/or dysfunction of retinal cells.
 XX
 PS Example; Page 73; 97pp; English.
 XX
 CC The sequence is that of a functional derivative of human insulin-like
 CC growth factor (IGF)-II which promotes the survival of retinal neuronal
 CC cells. It can be used for the treatment of retinal neuronal tissues which
 CC are suffering from the effects of injury, ageing and/or disease such as
 CC photodegeneration, trauma, axotomy, neurotoxic-excitatory degeneration,
 CC ischemic neuronal degeneration, inherited retinal dystrophy, diabetic
 CC retinopathy, Alzheimer's disease, infantile malignant osteopetrosis,
 CC ceroid lipofuscosin or cholestasis. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
 |||
 Db 8 AKS 10

RESULT 43

AAR42959

ID AAR42959-standard; peptide; 11-AA.

XX

AC AAR42959;

XX

DT 14-MAY-2003 (revised)

DT 25-MAR-2003 (revised)

DT 08-DEC-1993 (first entry)

XX

DE Beta chain VDJ region (Vbeta3-Jbeta1.1).

XX

KW CDR; T-cell receptor; TCR; vaccine.

XX

OS Synthetic.

XX

PN WO9312814-A2.
 XX
 PD 08-JUL-1993.
 XX
 PF 21-DEC-1992; 92WO-US011159.
 XX
 PR 24-DEC-1991; 91US-00813867.
 XX
 PA (IMMU-) IMMUNE RESPONSE CORP.
 XX
 PI Howell MD, Brostoff SW, Carlo DJ;
 XX
 DR WPI; 1993-227059/28.
 XX
 PT Vaccine comprising T cell receptor from T cells which mediate pathology -
 PT for treating and preventing T cell lymphoma, rheumatoid arthritis,
 PT auto:immune diseases etc.
 XX
 PS Claim 13; Page 73; 79pp; English.
 XX
 CC A vaccine for preventing or treating a T-cell mediated pathology in a
 CC vertebrate comprises a medium and a pure T-cell receptor (TCR) or
 CC immunogenic fragment corresp. to a TCR present on the surface of T- cells
 CC mediating the pathology. The immunogenic fragment may comprise the amino
 CC acid sequence of a beta-chain variable region, pref. the CD2 region (see
 CC Features Table of AAR38720-22). Alternatively the fragment may comprise
 CC the amino acid sequence of a beta-chain VDJ region of the TCR. The beta-
 CC chain VDJ region may comprise the sequences given in AAR42956-61.
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 14-MAY-2003 to
 CC correct PS field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 2 SSL 4

RESULT 44

AAR42956
 ID AAR42956 standard; peptide; 11 AA.
 XX
 AC AAR42956;
 XX
 DT 14-MAY-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 08-DEC-1993 (first entry)
 XX
 DE Beta chain VDJ region (Vbeta14-Jbeta2.1).
 XX
 KW CDR; T-cell receptor; TCR; vaccine.
 XX
 OS Synthetic.

XX
 PN WO9312814-A2.
 XX
 PD 08-JUL-1993.
 XX
 PF 21-DEC-1992; 92WO-US011159.
 XX
 PR 24-DEC-1991; 91US-00813867.
 XX
 PA (IMMU-) IMMUNE RESPONSE CORP.
 XX
 PI Howell MD, Brostoff SW, Carlo DJ;
 XX
 DR WPI; 1993-227059/28.
 XX
 PT Vaccine comprising T cell receptor from T cells which mediate pathology -
 PT for treating and preventing T cell lymphoma, rheumatoid arthritis,
 PT auto:immune diseases etc.
 XX
 PS Claim 12; Page 73; 79pp; English.
 XX
 CC A vaccine for preventing or treating a T-cell mediated pathology in a
 CC vertebrate comprises a medium and a pure T-cell receptor (TCR) or
 CC immunogenic fragment corresp. to a TCR present on the surface of T- cells
 CC mediating the pathology. The immunogenic fragment may comprise the amino
 CC acid sequence of a beta-chain variable region, pref. the CD2 region (see
 CC Features Table of AAR38720-22). Alternatively the fragment may comprise
 CC the amino acid sequence of a beta-chain VDJ region of the TCR. The beta-
 CC chain VDJ region may comprise the sequences given in AAR42956-61.
 CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 14-MAY-2003 to
 CC correct PS field.)
 XX
 SQ Sequence 11 AA;

 Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 8 SSL 10
 |||
 Db 2 SSL 4

RESULT 45

AAR32352

ID AAR32352 standard; peptide; 11 AA.

XX

AC AAR32352;

XX

DT 05-JUL-1993 (first entry)

XX

DE Human Factor X peptide.

XX

KW Anticoagulant; intrinsic; extrinsic; prothrombin activation; thrombin;
 KW formation; Factor Xa; pathway mediated activation; inhibition.

XX

OS Synthetic.

XX
 PN US5187155-A.
 XX
 PD 16-FEB-1993.
 XX
 PF 23-JUN-1989; 89US-00371561.
 XX
 PR 23-JUN-1989; 89US-00371561.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Fair DS;
 XX
 DR WPI; 1993-075751/09.
 XX
 PT Compsns. comprising peptide(s) of 10-50 aminoacid residues - inhibit
 PT factor X activation and/or Factor Xa function, useful for preventing
 PT blood clot formation and treating deep vein thrombosis, pulmonary
 PT embolism, etc.
 XX
 PS Example; Page 6; 23pp; English.
 XX
 CC The sequence is that of a peptide corresponding to amino acids 404-414 of
 CC the human factor X molecule which was tested for its effect, (as a % of
 CC the control rate), on the rate of Factor Xa formation and on the rate of
 CC thrombin formation. The results obt'd. were for activation of Factor X by
 CC the extrinsic activation complex 78%, by the intrinsic activation complex
 CC 98%, and activation by RVV-X, 76%. For the rate of thrombin formation the
 CC rate was 88% as compared to the control rate
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RKG 6
 |||
 Db 2 RKG 4

RESULT 46

AAR43594

ID AAR43594-standard; peptide; 11 AA.

XX

AC AAR43594;

XX

DT 25-MAR-2003 (revised)

DT 10-MAY-1994 (first entry)

XX

DE Peptide derived from insulin-like growth factor.

XX

KW IGF; IGF-II; neuronal cell survival; neurite regeneration; stroke;

KW epilepsy; Parkinson's disease; head injury; spinal cord injury;

KW age-related neuronal loss; amyotrophic lateral sclerosis.

XX

OS Synthetic.

XX
 PN WO9320836-A1.
 XX
 PD 28-OCT-1993.
 XX
 PF 14-APR-1993; 93WO-US003515.
 XX
 PR 15-APR-1992; 92US-00869913.
 PR 07-OCT-1992; 92US-00958903.
 XX
 PA (CEPH-) CEPHALON INC.
 XX
 PI Lewis ME, Kauer JC, Smith KR, Callison KV, Baldino F, Neff N;
 PI Iqbal M;
 XX
 DR WPI; 1993-351361/44.
 XX
 PT Peptide(s) derived from insulin-like growth factor - used for promoting
 PT neuronal cell survival and neurite regeneration, partic. in treating
 PT diseases e.g. stroke, epilepsy, Parkinson's, etc.
 XX
 PS Claim 12; Page 77; 119pp; English.
 XX
 CC The sequence is that of a fragment of insulin-like growth factor II (IGF-
 CC II). The synthetic peptide can be used to enhance the survival of
 CC neuronal cells in a mammal that are at risk of dying or to treat a head
 CC or spinal cord injury, or to enhance neurite regeneration in a mammal, or
 CC to treat stroke, epilepsy, age-related neuronal loss, amyotrophic lateral
 CC sclerosis and Parkinson's disease. See also AAR43590-645. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
 |||
 Db 8 AKS 10

RESULT 47

AAR43598

ID AAR43598 standard; peptide; 11 AA.
 XX
 AC AAR43598;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-MAY-1994 (first entry)
 XX
 DE Peptide derived from insulin-like growth factor.
 XX
 KW IGF; IGF-II; neuronal cell survival; neurite regeneration; stroke;
 KW epilepsy; Parkinson's disease; head injury; spinal cord injury;
 KW age-related neuronal loss; amyotrophic lateral sclerosis; cyclic.
 XX

OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1. .11
 XX
 PN WO9320836-A1.
 XX
 PD 28-OCT-1993.
 XX
 PF 14-APR-1993; 93WO-US003515.
 XX
 PR 15-APR-1992; 92US-00869913.
 PR 07-OCT-1992; 92US-00958903.
 XX
 PA (CEPH-) CEPHALON INC.
 XX
 PI Lewis ME, Kauer JC, Smith KR, Callison KV, Baldino F, Neff N;
 PI Iqbal M;
 XX
 DR WPI; 1993-351361/44.
 XX
 PT Peptide(s) derived from insulin-like growth factor - used for promoting
 PT neuronal cell survival and neurite regeneration, partic. in treating
 PT diseases e.g. stroke, epilepsy, Parkinson's, etc.
 XX
 PS Claim 15; Page 79; 119pp; English.
 XX
 CC The sequence is that of a fragment of insulin-like growth factor II (IGF-
 CC II). The synthetic peptide can be used to enhance the survival of
 CC neuronal cells in a mammal that are at risk of dying or to treat a head
 CC or spinal cord injury, or to enhance neurite regeneration in a mammal, or
 CC to treat stroke, epilepsy, age-related neuronal loss, amyotrophic lateral
 CC sclerosis and Parkinson's disease. See also AAR43590-645. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
 |||
 Db 7 AKS-9

RESULT 48
 AAR43618
 ID AAR43618 standard; peptide; 11 AA.
 XX
 AC AAR43618;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-MAY-1994 (first entry)
 XX
 DE Peptide derived from insulin-like growth factor.
 XX

KW IGF; IGF-II; neuronal cell survival; neurite regeneration; stroke;
 KW epilepsy; Parkinson's disease; head injury; spinal cord injury;
 KW age- related neuronal loss; amyotrophic lateral sclerosis; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1. .11
 XX
 PN WO9320836-A1.
 XX
 PD 28-OCT-1993.
 XX
 PF 14-APR-1993; 93WO-US003515.
 XX
 PR 15-APR-1992; 92US-00869913.
 PR 07-OCT-1992; 92US-00958903.
 XX
 PA (CEPH-) CEPHALON INC.
 XX
 PI Lewis ME, Kauer JC, Smith KR, Callison KV, Baldino F, Neff N;
 PI Iqbal M;
 XX
 DR WPI; 1993-351361/44.
 XX
 PT Peptide(s) derived from insulin-like growth factor - used for promoting
 PT neuronal cell survival and neurite regeneration, partic. in treating
 PT diseases e.g. stroke, epilepsy, Parkinson's, etc.
 XX
 PS Claim 20; Page 86; 119pp; English.
 XX
 CC The sequence is that of a fragment of insulin-like growth factor II (IGF-
 CC II). The synthetic peptide can be used to enhance the survival of
 CC neuronal cells in a mammal that are at risk of dying or to treat a head
 CC or spinal cord injury, or to enhance neurite regeneration in a mammal, or
 CC to treat stroke, epilepsy, age-related neuronal loss, amyotrophic lateral
 CC sclerosis and Parkinson's disease. See also AAR43590-645. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
 |||
 Db 7 AKS 9

RESULT 49
 AAR43599
 ID AAR43599 standard; peptide; 11 AA.
 XX
 AC AAR43599;
 XX
 DT 25-MAR-2003 (revised)

DT 10-MAY-1994 (first entry)
 XX
 DE Peptide derived from insulin-like growth factor.
 XX
 KW IGF; IGF-II; neuronal cell survival; neurite regeneration; stroke;
 KW epilepsy; Parkinson's disease; head injury; spinal cord injury;
 KW age- related neuronal loss; amyotrophic lateral sclerosis; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1. .11
 XX
 PN WO9320836-A1.
 XX
 PD 28-OCT-1993.
 XX
 PF 14-APR-1993; 93WO-US003515.
 XX
 PR 15-APR-1992; 92US-00869913.
 PR 07-OCT-1992; 92US-00958903.
 XX
 PA (CEPH-) CEPHALON INC.
 XX
 PI Lewis ME, Kauer JC, Smith KR, Callison KV, Baldino F, Neff N;
 PI Iqbal M;
 XX
 DR WPI; 1993-351361/44.
 XX
 PT Peptide(s) derived from insulin-like growth factor - used for promoting
 PT neuronal cell survival and neurite regeneration, partic. in treating
 PT diseases e.g. stroke, epilepsy, Parkinson's, etc.
 XX
 PS Claim 17; Page 79; 119pp; English.
 XX
 CC The sequence is that of a fragment of insulin-like growth factor II (IGF-
 CC II). The synthetic peptide can be used to enhance the survival of
 CC neuronal cells in a mammal that are at risk of dying or to treat a head
 CC or spinal cord injury, or to enhance neurite regeneration in a mammal, or
 CC to treat stroke, epilepsy, age-related neuronal loss, amyotrophic lateral
 CC sclerosis and Parkinson's disease. See also AAR43590-645. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
 |||
 Db 7 AKS 9

RESULT 50
 AAR43638
 ID AAR43638 standard; peptide; 11 AA.

XX
 AC AAR43638;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-MAY-1994 (first entry)
 XX
 DE Peptide derived from insulin-like growth factor.
 XX
 KW IGF; IGF-II; neuronal cell survival; neurite regeneration; stroke;
 KW epilepsy; Parkinson's disease; head injury; spinal cord injury;
 KW age- related neuronal loss; amyotrophic lateral sclerosis; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1. .11
 FT Modified-site 3
 FT /note= "D form"
 XX
 PN WO9320836-A1.
 XX
 PD 28-OCT-1993.
 XX
 PF 14-APR-1993; 93WO-US003515.
 XX
 PR 15-APR-1992; 92US-00869913.
 PR 07-OCT-1992; 92US-00958903.
 XX
 PA (CEPH-) CEPHALON INC.
 XX
 PI Lewis ME, Kauer JC, Smith KR, Callison KV, Baldino F, Neff N;
 PI Iqbal M;
 XX
 DR WPI; 1993-351361/44.
 XX
 PT Peptide(s) derived from insulin-like growth factor - used for promoting
 PT neuronal cell survival and neurite regeneration, partic. in treating
 PT diseases e.g. stroke, epilepsy, Parkinson's, etc.
 XX
 PS Claim 16; Page 93; 119pp; English.
 XX
 CC The sequence is that of a fragment of insulin-like growth factor II (IGF-
 CC II). The synthetic peptide can be used to enhance the survival of
 CC ~~neuronal cells in a mammal that are at risk of dying or to treat a head~~
 CC or spinal cord injury, or to enhance neurite regeneration in a mammal, or
 CC to treat stroke, epilepsy, age-related neuronal loss, amyotrophic lateral
 CC sclerosis and Parkinson's disease. See also AAR43590-645. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

 Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 AKS 3
 |||

RESULT 51

AAR37430

ID AAR37430 standard; peptide; 11 AA.

XX

AC AAR37430;

XX

DT 25-MAR-2003 (revised)

DT 08-SEP-1993 (first entry)

XX

DE Promega peptide 5.

XX

KW Modified peptide substrate; non-radioactive; detection; dansyl;
KW sulphorhodamine 101; lissamine; rhodamine; enzymes; phosphatases;
KW protein kinases; proteases.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "detection tag= lissamine, Rhodamine"

XX

PN WO9310461-A1.

XX

PD 27-MAY-1993.

XX

PF 12-NOV-1992; 92WO-US009595.

XX

PR 12-NOV-1991; 91US-00791928.

XX

PA (PROM-) PROMEGA CORP.

XX

PI Shultz JW, White DH;

XX

DR WPI; 1993-182698/22.

XX

PT Quantitating presence or activity of enzyme - by incubating with modified
PT peptide substrate and measuring the modified peptide prod.

XX

PS Claim 24; Page 27; 103pp; English.

XX

~~CC Promega peptide 5 is tagged with dansyl at residue 1 and may be used in a~~
CC novel non-radioactive method of quantitating the presence or activity of
CC an enzyme. The method can be used for rapid, specific and highly
CC sensitive detection of enzymes such as protein kinases, phosphatases and
CC proteases, esp. in this case protein kinase C. They can be used to study
CC enzyme function in metabolism and in diagnosis of disease. They also
CC allow quantitative determ. of the enzyme's activity. See also AAR37426-
CC 36. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KSR 4
 | | |
Db 6 KSR 8

RESULT 52

AAR44560

ID AAR44560 standard; protein; 11 AA.

XX

AC AAR44560;

XX

DT 25-MAR-2003 (revised)

DT 26-MAY-1994 (first entry)

XX

DE Encoded by human Ews exon7/Hum-Fli-1 exon 5 fusion.

XX

KW chromosomal translocation; chimeric; chimaeric; Ewing sarcoma; Ews gene;

KW malignant melanoma; hum-fli-1;

KW primitive peripheral neuroectodermal tumour; human chromosome 11;

KW human chromosome 22.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 1. .5

FT /note= "encoded by 3'-end of Ews exon 7"

FT Region 6. .11

FT /note= "encoded by 5'-end of Hum-Fli-1 exon 5"

XX

PN WO9323549-A2.

XX

PD 25-NOV-1993.

XX

PF 19-MAY-1993; 93WO-FR000494.

XX

PR 20-MAY-1992; 92FR-00006123.

XX

PA (CNRS) CNRS CENT NAT RECH SCI.

XX

PI Aurias A, Delattre O, Desmaze C, Melot T, Peter M, Plougastel B;

PI Thomas G, Zucman J;

XX

DR WPI; 1993-386580/48.

DR N-PSDB; AAQ50673.

XX

PT New nucleic acid of EWS gene and its hybrid(s) - contg. gene sequence

PT involved in chromosomal trans-location, also derived mRNA, probes, fusion

PT proteins etc., for diagnosis and treatment of Ewing sarcoma and melanoma.

XX

PS Disclosure; Fig 14; 123pp; French.

XX

CC The intron-exon junctions of the human Ews gene and the Hum-Fli-1 gene

CC have been sequenced (see AAQ50646 and AAQ50662, respectively). The

CC different fusion products which could be formed by fusing exons from the

CC two genes, as happens after specific chromosomal translocations, can be

CC predicted. See AAR44558-R44565 for the amino acid sequences resulting

CC from the different fusion events. (Updated on 25-MAR-2003 to correct PN
CC field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10

|||

Db 6 SSL 8

RESULT 53

AAR53641

ID AAR53641 standard; protein; 11 AA.

XX

AC AAR53641;

XX

DT 25-MAR-2003 (revised)

DT 19-JAN-1995 (first entry)

XX

DE Mutant transaminase tyrB fragment from pIF200.

XX

KW improved method; transaminases; conversion; D-amino acids; L-amino acids;

KW tyr B; tyrosine aminotransferase; amino acid synthesis.

XX

OS Escherichia coli.

XX

PN US5316943-A.

XX

PD 31-MAY-1994.

XX

PF 19-JUN-1989; 89US-00368480.

XX

PR 14-JUN-1988; 88US-00206622.

XX

PA (SCOL/) SCOLLAR M P.

PA (KIDM/) KIDMAN G E.

PA (ROBI/) ROBINSON L E.

PA (ROBI/) ROBINSON L E.

XX

PI Fotheringham IG, Kidman GE, Robinson LE, Scollar MP;

XX

DR WPI; 1994-176276/21.

DR N-PSDB; AAQ63803.

XX

PT Prodn. of optically pure L-aminoacid from D,L racemic mixt. - by

PT fermentation with microorganism producing recombinant amino:transferase

PT to convert D to L isomer, for use in prodn. of L-phenylalanine for prepn.

PT of aspartame sweetener.

XX

PS Disclosure; Fig 4; 9pp; English.

XX

CC The method of the invention is particularly useful in the prepn. of

CC aspartame, the low calorie sweetener. It is preferred to separate the two

CC isomers or convert a racemic mixture of the two to obtain one of the
 CC enantiomers that is relatively free of contamination by the other.
 CC Aspartame is a dipeptide comprising aspartic acid and phenylalanine
 CC (Phe), in the L-L form. Methods of production of Phe typically result in
 CC racemic mixtures of D and L isomers which must either be separated or
 CC resolved, to yield pure L-Phe. L-amino acids can be produced by
 CC transamination. The enzymes used are expensive and often inactivated by
 CC hydrogen peroxide (a byproduct of the reaction). This invention provides
 CC a transaminase that produces optically pure L-Phe from a D,L racemic
 CC mixture without the problems of previous methods. More specifically the
 CC enzyme of interest is a mutant of the tyrosine transaminase (AAR53641 and
 CC AAR53642, encoded by the tyrB gene - AAQ63803-4). (Updated on 25-MAR-2003
 CC to correct PF field.)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9

|||

Db 2 NSS 4

RESULT 54

AAR52885

ID AAR52885 standard; peptide; 11 AA.

XX

AC AAR52885;

XX

DT 25-MAR-2003 (revised)

DT 07-NOV-1994 (first entry)

XX

DE TK-SH2 association inhibitory peptide.

XX

KW Tyrosine kinase; SH2 domains; inhibition of association; abl;

KW Epidermal Growth Factor Receptor; phosphotyrosine residue;

KW control proliferative disease; control cancer; TK; EGFR;

KW Src-homology domains.

XX

OS Synthetic.

XX

Key	Location/Qualifiers
FT Modified-site	4
FT	/label= other
FT	/note= "phosphotyrosine"

XX

PN W09407913-A1.

XX

PD 14-APR-1994.

XX

PF 22-SEP-1993; 93WO-US008996.

XX

PR 25-SEP-1992; 92US-00951241.

PR 15-SEP-1993; 93US-00122028.

XX

PA (WARN) WARNER LAMBERT CO.
 XX
 PI Dobrusin EM, Mcnamara DJ, Soltiel AR, Maclean D, Thieme-Sefler A;
 XX
 DR WPI; 1994-135508/16.
 XX
 PT New peptide(s) with a tyrosine auto-phosphorylation site - inhibit
 PT tyrosine kinase association with regulatory proteins, used for treating,
 PT e.g., hyper-proliferative, viral, allergic inflammatory, auto-immune and
 PT cardiovascular diseases.
 XX
 PS Example 7; Page 11; 50pp; English.
 XX
 CC The peptide inhibits the association of a tyrosine kinase with its
 CC cellular substrates and effectively uncouples the tyrosine kinase from
 CC specific signal transduction pathways. The peptide inhibition is probably
 CC the result of competition between the phosphorylated peptide and the
 CC phosphorylated receptor for the same binding site on the SH2 domains. The
 CC inventors claim the peptides can be used for the control of several
 CC proliferative diseases, eg. cancer. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
 |||
 Db 9 NSS 11

RESULT 55

AAR52886

ID AAR52886 standard; peptide; 11 AA.
 XX
 AC AAR52886;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-NOV-1994 (first entry)
 XX
 DE TK-SH2 association inhibitory peptide.

KW Tyrosine kinase; SH2 domains; inhibition of association; abl;
 KW Epidermal Growth Factor Receptor; phosphotyrosine residue;
 KW control proliferative disease; control cancer; TK; EGFR;
 KW Src-homology domains.

XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Modified-site 5
 FT /label= other
 FT /note= "phosphotyrosine"
 XX
 PN WO9407913-A1.

XX
PD 14-APR-1994.
XX
PF 22-SEP-1993; 93WO-US008996.
XX
PR 25-SEP-1992; 92US-00951241.
PR 15-SEP-1993; 93US-00122028.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Dobrusin EM, Mcnamara DJ, Soltiel AR, Maclean D, Thieme-Sefler A;
XX
DR WPI; 1994-135508/16.
XX
PT New peptide(s) with a tyrosine auto-phosphorylation site - inhibit
PT tyrosine kinase association with regulatory proteins, used for treating,
PT e.g., hyper-proliferative, viral, allergic inflammatory, auto-immune and
PT cardiovascular diseases.
XX
PS Example 8; Page 11; 50pp; English.
XX
CC The peptide inhibits the association of a tyrosine kinase with its
CC cellular substrates and effectively uncouples the tyrosine kinase from
CC specific signal transduction pathways. The peptide inhibition is probably
CC the result of competition between the phosphorylated peptide and the
CC phosphorylated receptor for the same binding site on the SH2 domains. The
CC inventors claim the peptides can be used for the control of several
CC proliferative diseases, eg. cancer. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
| | |
Db 9 NSS 11

RESULT 56

AAR68593

ID AAR68593-standard; peptide; 11-AA.

XX

AC AAR68593;

XX

DT 25-MAR-2003 (revised)

DT 01-SEP-1995 (first entry)

XX

DE Rat NDF peptide fragment #3.

XX

KW Alpha; beta; neu differentiation factor; NDF; human; rat; p185-neu;
KW tyrosine phosphorylation; differentiation; phenotype; proliferation;
KW wound; tumour; epithelial tissue; breast; stomach; PCR; amplify;
KW gastrointestinal disease; Barrett's oesophagus; primer;
KW (non-)cystic kidney disease; inflammatory bowel disease.

XX
 OS Rattus rattus.
 XX
 PN WO9428133-A1.
 XX
 PD 08-DEC-1994.
 XX
 PF 23-MAY-1994; 94WO-US005769.
 XX
 PR 21-MAY-1993; 93US-00066384.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Wen D, Koski RA, Pierce GF, Hu S, Sugarman BJ, Liu N;
 XX
 DR WPI; 1995-022805/03.
 XX
 PT New recombinant neu differentiation factors and corresp. DNA - are used
 PT in the treatment of tumours, dermal wounds, and gastrointestinal, kidney
 PT and inflammatory bowel diseases.
 XX
 PS Example 1; Page 226; 34lpp; English.
 XX
 CC The sequences given in AAR68591-95 represent fragments of rat neu
 CC differentiation factor (NDF). NDF peptides possess the ability to
 CC stimulate p185-neu tyrosine phosphorylation. These peptides have the
 CC ability to induce a differentiated phenotype in certain cell lines and
 CC can stimulate or inhibit proliferation of certain cell lines. NDF's can
 CC be used to treat wounds, tumours derived from epithelial tissue of the
 CC breast, stomach etc., gastrointestinal disease, Barrett's oesophagus,
 CC (non-)cystic kidney disease or inflammatory bowel disease. DNA sequences
 CC derived from these peptides may be used as primers and probes in the
 CC isolation sequences from human cDNA libraries which encode human NDF's.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

 Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 8 SSL 10
 |||
 Db 8-SSL-10

RESULT 57

AAR78518

ID AAR78518 standard; peptide; 11 AA.

XX

AC AAR78518;

XX

DT 25-JAN-1996 (first entry)

XX

DE Synthetic HTLV peptide #50 binds to HLA-B35 antigen.

XX

KW Human T-cell leukaemia virus; HTLV; cytotoxic; HLA-B35 antigen; vaccine;

KW prophylaxis; HTLV-1 associated myelopathy; HAM.
 XX
 OS Synthetic.
 XX
 PN JP07126290-A.
 XX
 PD 16-MAY-1995.
 XX
 PF 29-OCT-1993; 93JP-00294472.
 XX
 PR 29-OCT-1993; 93JP-00294472.
 XX
 PA (KENB/) KENBARA K.
 PA (TAKI/) TAKIGUCHI M.
 XX
 DR WPI; 1995-212957/28.
 XX
 PT Synthetic peptide(s) derived from human T cell leukaemia virus (HTLV) -
 PT bind to HLA-B35 antigen, useful in a vaccine against HTLV-1 associated
 PT myelopathy and human T cell leukaemia.
 XX
 PS Claim 1; Page 2; 13pp; Japanese.
 XX
 CC Peptides AAR78469-R78518 are synthetic peptides derived from the sequence
 CC of the human T-cell leukaemia virus (HTLV) which are capable of inducing
 CC cytotoxic T cells by binding to the HLA-B35 antigen. The peptides can be
 CC used as a vaccine in prophylaxis of human T cell leukaemia and HTLV-1
 CC associated myelopathy (HAM), both caused by HTLV. This sequence
 CC corresponds to amino acids 97-107 of the HTLV-1a and c strains pol
 CC protein
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 5 SSL 7

RESULT 58

AAW21497

ID AAW21497 standard; peptide; 11 AA.
 XX
 AC AAW21497;
 XX
 DT 16-OCT-2003 (revised)
 DT 30-JUL-1997 (first entry)
 XX
 DE Hepatitis delta antigen derived signal oligopeptide #2.
 XX
 KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
 KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;

KW gonadoliberin precursor; plasminogen activator inhibitor 2; prorenin;
KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX

OS Hepatitis D virus.

XX

PN WO9519568-A1.

XX

PD 20-JUL-1995.

XX

PF 12-JAN-1995; 95WO-US000575.

XX

PR 14-JAN-1994; 94US-00182248.

XX

PA (RATH/) RATH M.

XX

PI Rath M;

XX

DR WPI; 1995-263953/34.

XX

PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT regions of max. hydrophilicity, used in modulating communication between
PT protein(s).

XX

PS Claim 5; Page 72; 88pp; English.

XX

CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC peptides. These signal oligopeptides are localised on the surface of the
CC protein and are represented by the hydrophilicity maxima of the protein.
CC These peptides are enriched in charged amino acids arranged with neutral
CC spacer amino acids. The specific signal character of these oligopeptides
CC is determined by a characteristic combination of conformation and charge
CC within the signal sequence. These oligopeptides may be used as vaccines
CC in the treatment of human disease, as competitive inhibitors to prevent
CC or reduce the metabolic action or interaction of a selected protein by
CC blocking its specific signal sequences, or as therapeutic agents to
CC function as feedback regulators to reduce synthesis rate of a selected
CC protein. These peptides may be modified by omitting one or more amino
CC acids at the N- and/or C-terminal, by substituting one or more amino
CC ~~acids without consideration of charge and polarity, by substituting one~~
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these.
CC (Updated on 16-OCT-2003 to standardise OS field)

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5

|||

Db 2 SRK 4

RESULT 59

AAW21210

ID AAW21210 standard; peptide; 11 AA.

XX

AC AAW21210;

XX

DT 29-JUL-1997 (first entry)

XX

DE Farnesyl synthetase derived signal oligopeptide #10.

XX

KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;
 KW competitive inhibitor; feedback regulator; synthesis; gastrin precursor;
 KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
 KW gonadoliberein precursor; plasminogen activator inhibitor 2; prorenin;
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
 KW Treponema pallidum membrane protein; TMPA; islet amyloid polypeptide;
 KW fibroblast MMP1; schistosoma elastase precursor; schistosomin;
 KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.

XX

OS Homo sapiens.

XX

PN WO9519568-A1.

XX

PD 20-JUL-1995.

XX

PF 12-JAN-1995; 95WO-US000575.

XX

PR 14-JAN-1994; 94US-00182248.

XX

PA (RATH/) RATH M.

XX

PI Rath M;

XX

DR WPI; 1995-263953/34.

XX

PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
 PT regions of max. hydrophilicity, used in modulating communication between
 PT protein(s).

XX

PS Claim 5; Page 24; 88pp; English.

XX

CC The sequences given in AAW21201-560 represent hydrophilic signal oligo-
 CC peptides. These signal oligopeptides are localised on the surface of the
 CC protein and are represented by the hydrophilicity maxima of the protein.
 CC These peptides are enriched in charged amino acids arranged with neutral
 CC spacer amino acids. The specific signal character of these oligopeptides
 CC is determined by a characteristic combination of conformation and charge
 CC within the signal sequence. These oligopeptides may be used as vaccines
 CC in the treatment of human disease, as competitive inhibitors to prevent
 CC or reduce the metabolic action or interaction of a selected protein by
 CC blocking its specific signal sequences, or as therapeutic agents to
 CC function as feedback regulators to reduce synthesis rate of a selected

CC protein. These peptides may be modified by omitting one or more amino
CC acids at the N- and/or C-terminal, by substituting one or more amino
CC acids without consideration of charge and polarity, by substituting one
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10
|||
Db 6 SSL 8

RESULT 60

AAR98482

ID AAR98482 standard; peptide; 11 AA.

XX

AC AAR98482;

XX

DT 12-OCT-1996 (first entry)

XX

DE Anti-IL-5 MAb heavy chain variable region CDR3.

XX

KW Antibody engineering; humanised antibody; chimeric antibody; Fab;

KW interleukin-5; IL-5; eosinophil; asthma; therapy; diagnosis;

KW complementarity determining region; CDR; heavy chain; VH;

KW monoclonal antibody; MAb.

XX

OS Mus sp.

XX

PN W09621000-A2.

XX

PD 11-JUL-1996.

XX

PF 22-DEC-1995; 95WO-US017082.

XX

PR 23-DEC-1994; 94US-00363131.

PR 06-JUN-1995; 95US-00467420.

PR 06-JUN-1995; 95US-00470110.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Ames RS, Appelbaum ER, Chaiken IM, Cook RM, Gross MS, Holmes SD;

PI Mcmillan LJ, Theisen TW;

XX

DR WPI; 1996-333976/33.

XX

PT New monoclonal antibody to human interleukin-5 - used to produce products

PT for the treatment and diagnosis of conditions associated with excess

PT eosinophil prodn., e.g asthma etc.

XX

PS Claim 11; Page 48; 120pp; English.

XX
 CC The complementarity determining regions (CDRs) for the VH region of
 CC monoclonal antibody (MAb) 2B6 (see also AAR98478) are given in AAR98480-
 CC 82. MAb 2F2 VH (see also AAR98478) had identical CDRs. For MAb 2E3 VH
 CC (see also AAR98496), CDR1 and CDR2 are identical to those of 2B6 and 2F2,
 CC but CDR3 has a different amino acid sequence (AAR98483). The CDRs for the
 CC 2B6 VL region (see also AAR98479) are given in AAR98484-86. For 2F2 VL
 CC (see also AAR98495) and 2E3 VL (see also AAR98497), CDR1 and CDR2 are
 CC identical to CDR1 and CDR2 of 2B6, but CDR3 is different (AAR98487). 2B6,
 CC 2F2 and 2E3 are murine anti-human interleukin-5 MAb's. The CDRs can be
 CC used in the construction of humanised antibodies (see also AAR98488-89)
 CC and AAR98492-93) useful in the treatment of IL-5-mediated conditions,
 CC e.g. asthma
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 4 SSL 6

RESULT 61

AAW05770

ID AAW05770 standard; peptide; 11 AA.

XX

AC AAW05770;

XX

DT 25-MAR-2003 (revised)

DT 28-JUL-1997 (first entry)

XX

DE Presenilin-1-1 residues 50-60.

XX

KW Presenilin-1; human; hPS1-1; hPS1-2; PS-2; integral membrane protein; AD;

KW familial Alzheimer's disease; cerebral haemorrhage; schizophrenia;

KW depression; antibody; gene expression modulator; therapy; mutagen.

XX

OS Homo sapiens.

XX

PN WO9634099-A2.

XX

PD 31-OCT-1996.

XX

PF 29-APR-1996; 96WO-CA000263.

XX

PR 28-APR-1995; 95US-00431048.

PR 28-JUN-1995; 95US-00496841.

PR 31-JUL-1995; 95US-00509359.

XX

PA (HSCR-) HSC RES & DEV LP.

PA (UTOR) UNIV TORONTO GOVERNING COUNCIL.

XX

PI St George's Hospital, Fraser PE, Rommens JM;

XX

DR WPI; 1996-497631/49.
 XX
 PT New presenilin genes - useful for diagnosis, therapy and drug screening
 PT of familial Alzheimer's disease, cerebral disorders, etc.
 XX
 PS Claim 71; Page; 178pp; English.
 XX
 CC AAW05768-W05788 represent antigenic fragments of the human presenilin-1-1
 CC protein (see AAW05733 for wild type sequence). AAW05734 represents a
 CC different wild type form of presenilin-1 that results from alternate
 CC splicing of the genomic DNA sequence. The presenilins are a family of
 CC highly conserved integral membrane proteins with a common structural
 CC motif, common alternate splicing patterns, and common mutational hot spot
 CC regions. Mutations in PS genes are implicated in familial Alzheimer's
 CC disease (AD) and possibly other diseases such as cerebral haemorrhage,
 CC schizophrenia, depression etc., so detection of mutations in the DNA
 CC encoding the wild type sequences can be used for diagnosis of these
 CC diseases. The wild type proteins, or vectors that express them or
 CC containing antisense sequences, antibodies selective for these mutant
 CC forms of the proteins and modulators of PS gene expression are
 CC potentially useful for treatment of AD etc. Transgenic animals are useful
 CC as models for drug screening. The antibodies can also be used e.g. for
 CC affinity purification and in immunoassays. (Updated on 25-MAR-2003 to
 CC correct PI field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GNS 8
 |||
 Db 8 GNS 10

RESULT 62

AAR89702

ID AAR89702 standard; peptide; 11 AA.

XX

AC AAR89702;

XX

DT 25-MAR-2003 (revised)

DT 02-SEP-1996 (first entry)

XX

DE Prostate specific antigen, semenogelin derived, cleavage substrate.

XX

KW Human; semenogelin I; sperm entrapping gel; ejaculation; protease;
 KW gel structure; dissolution; prostate specific antigen; proteolysis;
 KW chymotrypsin like specificity; peptide substrate; cleavage site; assay;
 KW determination; proteolytic activity; identification; inhibitor;
 KW cytotoxic agent; conjugated; treatment; prostate cancer.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "acylated"
 FT Cleavage-site 7. .8
 FT /note= "prostate specific antigen proteolytic cleavage
 FT site"
 FT Modified-site 11
 FT /note= "C-terminally conjugated to the amino of the sugar
 FT moiety of doxorubicin"
 XX
 PN WO9600503-A1.
 XX
 PD 11-JAN-1996.
 XX
 PF 07-JUN-1995; 95WO-US008156.
 XX
 PR 28-JUN-1994; 94US-00267092.
 PR 15-MAR-1995; 95US-00404833.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI DefeoJones D, Feng D, Garsky VM, Jones RE, Oliff AI;
 XX
 DR WPI; 1996-077275/08.
 XX
 PT New peptide substrates cleaved by prostate-specific antigen - also
 PT cytotoxic conjugates for treating prostate cancer, and assay for
 PT determination of PSA activity.
 XX
 PS Claim 19; Page 104; 142pp; English.
 XX
 CC Human semenogelin I (hSI) is one of the major proteins, including hSII
 CC and fibronectin, in the sperm entrapping gel formed at ejaculation. This
 CC gel structure undergoes dissolution via the action of prostate specific
 CC antigen (PSA), a protease with chymotrypsin like specificity, which
 CC proteolyses the above major proteins. New substrates, including the
 CC present peptide, cleaved by PSA, i.e. peptides contg. a hSI PSA cleavage
 CC site, can be used in assays to determine the proteolytic activity of free
 CC PSA in a sample, and to identify cpds. which inhibit the proteolytic
 CC activity of PSA, they may also be conjugated, via a covalent bond or
 CC peptide linker, to a cytotoxic agent and used to treat prostate cancer.
 CC In a PSA hydrolysis assay, the percentage of the present peptide cleaved
 CC by YORK PSA after 3 hrs. was 100 %. (Updated on 25-MAR-2003 to correct PI
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 9 SSL 11

RESULT 63
 AAR89705
 ID AAR89705 standard; peptide; 11 AA.

XX
 AC AAR89705;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-SEP-1996 (first entry)
 XX
 DE Prostate specific antigen, semenogelin derived, cleavage substrate.
 XX
 KW Human; semenogelin I; sperm entrapping gel; ejaculation; protease;
 KW gel structure; dissolution; prostate specific antigen; proteolysis;
 KW chymotrypsin like specificity; peptide substrate; cleavage site; assay;
 KW determination; proteolytic activity; identification; inhibitor;
 KW cytotoxic agent; conjugated; treatment; prostate cancer.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "acylated"
 FT Cleavage-site 7. .8
 FT /note= "prostate specific antigen proteolytic cleavage
 FT site"
 FT Modified-site 11
 FT /note= "C-terminally conjugated to the amino of the sugar
 FT moiety of doxorubicin"
 XX
 PN WO9600503-A1.
 XX
 PD 11-JAN-1996.
 XX
 PF 07-JUN-1995; 95WO-US008156.
 XX
 PR 28-JUN-1994; 94US-00267092.
 PR 15-MAR-1995; 95US-00404833.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI DefeoJones D, Feng D, Garsky VM, Jones RE, Oliff AI;
 XX
 DR WPI; 1996-077275/08.
 XX
 PT New peptide substrates cleaved by prostate-specific antigen - also
 PT cytotoxic conjugates for treating prostate cancer, and assay for
 PT determination of PSA activity.
 XX
 PS Example 3; Page 105; 142pp; English.
 XX
 CC Human semenogelin I (hSI) is one of the major proteins, including hSII
 CC and fibronectin, in the sperm entrapping gel formed at ejaculation. This
 CC gel structure undergoes dissolution via the action of prostate specific
 CC antigen (PSA), a protease with chymotrypsin like specificity, which
 CC proteolyses the above major proteins. New substrates, including the
 CC present peptide, cleaved by PSA, i.e. peptides contg. a hSI PSA cleavage
 CC site, can be used in assays to determine the proteolytic activity of free
 CC PSA in a sample, and to identify cpds. which inhibit the proteolytic
 CC activity of PSA, they may also be conjugated, via a covalent bond or
 CC peptide linker, to a cytotoxic agent and used to treat prostate cancer.

CC In a PSA hydrolysis assay, the percentage of the present peptide cleaved
CC by YORK PSA after 4 hrs. was 0 %. (Updated on 25-MAR-2003 to correct PI
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 9 SSL 11

RESULT 64

AAR98513

ID AAR98513 standard; peptide; 11 AA.

XX

AC AAR98513;

XX

DT 04-MAR-1997 (first entry)

XX

DE CD8 antagonist #8.

XX

KW CD8 antagonist; inhibitor; T-cell activation; human; CD8 alpha chain;

KW thymic differentiation; transplantation; bone marrow; liver; heart; lung;

KW kidney; cornea; skin graft; graft versus host disease; therapy.

XX

OS Synthetic.

XX

PN WO9622106-A1.

XX

PD 25-JUL-1996.

XX

PF 17-JAN-1996; 96WO-US000310.

XX

PR 17-JAN-1995; 95US-00372952.

XX

PA (UYJE-) UNIV JEFFERSON THOMAS.

XX

PI Jameson BA, Choksi S, Korngold R, Huang Z;

XX

DR WPI; 1996-354307/35.

XX

PT CD8 antagonist peptide(s) - used for inhibiting T cell activation,
PT partic. for treating transplant rejection or graft versus host disease.

XX

PS Example 1; Page 23; 44pp; English.

XX

CC AAR98506-R98513 represent CD8 antagonists of the invention. CD8 plays a
CC major role in the activation of mature T-cells, and in the thymic
CC differentiation process that leads to CD8 expression. CD8 is expressed
CC either as a homodimer (containing two alpha chains) or as a heterodimer
CC (an alpha and a beta chain). The CD8 CDR2-like region is involved in
CC regulating T-cell activation. The antagonists of the invention comprise a
CC molecular surface similar to at least a portion of human CD8 molecular

CC surface around the site of one of these peptides. The compounds of the
CC invention compete with CD8 so as to inhibit T-cell activation. They can
CC also be used to treat an individual who is about to undergo, is
CC undergoing, or has undergone a transplantation procedure such as bone
CC marrow, liver, heart, kidney, lung, islets, or cornea transplantation, or
CC skin grafts. The compounds can also be used to treat an individual
CC suspected of suffering from, or susceptible to graft versus host disease

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9

|||

Db 6 NSS 8

RESULT 65

AAW06895

ID AAW06895 standard; peptide; 11 AA.

XX

AC AAW06895;

XX

DT 19-JUN-1997 (first entry)

XX

DE Anti-CD18 Fab epitope.

XX

KW Anti-CD18; salvage receptor binding epitope; immunoglobulin G; IgG;

KW variant; kidney; in vivo half-life; effector; antigenic function;

KW LFA-1 antagonist; psoriasis; transplant rejection; asthma; wound repair;

KW meningitis; multiple sclerosis; B-cell lymphoma.

XX

OS Synthetic.

XX

PN WO9632478-A1.

XX

PD 17-OCT-1996.

XX

PF 28-MAR-1996; 96WO-US004316.

XX

PR 14-APR-1995; 95US-00422093.

XX

PA (GETH) GENENTECH INC.

XX

PI Presta LG, Snedecor BR;

XX

DR WPI; 1996-477129/47.

XX

PT Polypeptide variants, esp. LFA-1 antagonists, comprising a salvage

PT receptor binding epitope of an Fc region of an IgG - have increased in

PT vivo half-life and are useful to treat e.g. psoriasis, transplant

PT rejection, asthma, etc.

XX

PS Claim 13; Page 63; 72pp; English.

XX

CC This peptide sequence is that of an anti-CD18 Fab epitope, in particular
 CC a salvage receptor binding epitope of an immunoglobulin G (IgG) molecule.
 CC Polypeptide variants of a protein which is cleared from the kidney (and
 CC which does not contain a Fc region of a IgG) comprise the present
 CC sequence and possibly also one of AAW06896-99. The variant has a longer
 CC in vivo half-life and is useful for providing in vivo effector or
 CC antigenic function or activity. In partic. LFA-1 antagonist variants can
 CC be obtd. for treating LFA-1-mediated disorders (claimed), e.g. psoriasis,
 CC transplant rejection, asthma, wound repair, meningitis, multiple
 CC sclerosis or B-cell lymphomas
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
 |||
 Db 3 NSS 5

RESULT 66

AAR91286

ID AAR91286 standard; peptide; 11 AA.

XX

AC AAR91286;

XX

DT 14-OCT-1996 (first entry)

XX

DE Anti-idiotypic T-cell modulating peptide.

XX

KW Peptide; VDJ; anti-idiotypic T cell; vaccine; detection; diagnosis;
 KW insulin dependent diabetes mellitus; IDDM; assay; proliferation;
 KW cytokine.

XX

OS Synthetic.

XX

PN WO9611214-A1.

XX

PD 18-APR-1996.

XX

PF 10-OCT-1995; 95WO-US012686.

XX

PR 07-OCT-1994; 94IL-00111196.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Cohen IR, Elias D;

XX

DR WPI; 1996-209811/21.

XX

PT Novel VDJ peptide and corresponding DNA - used in treatment and
 PT prevention of insulin dependent diabetes mellitus.

XX

PS Claim 3; Page 41; 60pp; English.

XX

CC Peptides having a VDJ region where V includes the dipeptide sequence A-S,
 CC D preferably has 2-5 amino acids and includes the dipeptide L-G and J
 CC includes the tripeptide N-Q-D, may be used as agents for the detection of
 CC anti-idiotypic T-cells and in a vaccine against insulin dependent
 CC diabetes mellitus (IDDM). The peptides may also be used in the prevention
 CC and treatment of IDDM by activating autologous T- cells against the
 CC peptides and then re-administering them to the patient. The peptides may
 CC also be used in the diagnosis or staging of IDDM or for monitoring the
 CC course of treatment of IDDM by assaying T-cells of the subject being
 CC tested for proliferation or cytokine production upon in vitro contact
 CC with the peptides
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 2 SSL 4

RESULT 67

AAW09653

ID AAW09653 standard; peptide; 11 AA.

XX

AC AAW09653;

XX

DT 25-MAR-2003 (revised)

DT 20-MAY-1997 (first entry)

XX

DE Labelled peptide substrate used in enzyme activity assay.

XX

KW Enzyme activity; assay; measurement; label; rhodamine; dansyl;

KW non-radioactive; electrophoretic separation; protein kinase; protease;

KW phosphatase.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "labelled with rhodamine B detection tag"

XX

PN US5580747-A.

XX

PD 03-DEC-1996.

XX

PF 21-JAN-1994; 94US-00185448.

XX

PR 12-NOV-1991; 91US-00791928.

XX

PA (PROM-) PROMEGA CORP.

XX

PI White DH, Shultz JW;

XX

DR WPI; 1997-033568/03.

XX
PT Non:radioactive assay for measuring enzyme activity - involving
PT electrophoretic sepn. of labelled cleavage prod. from labelled peptide
PT substrate.
XX
PS Claim 5; Col 39-40; 35pp; English.
XX
CC AAW09653 is a peptide substrate used in a non-radioactive assay for
CC measuring enzyme activity. The assay comprises incubating the enzyme with
CC the labelled peptide substrate to form a labelled peptide product;
CC separating the product from the substrate by agarose gel electrophoresis
CC and measuring the amount of product by detecting the label by
CC fluorescence or chemiluminescence. The assay can be performed rapidly and
CC with great sensitivity. This peptide is especially for determining
CC protein kinase C activity, e.g. to study its function in metabolism or to
CC screen for potential inhibitors. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KSR 4
| | |
Db 6 KSR 8

RESULT 68

AAE22529

ID AAE22529 standard; peptide; 11 AA.

XX

AC AAE22529;

XX

DT 26-JUL-2002 (first entry)

XX

DE Human Fcgamma RI antibody (H22) hinge region fragment #3.

XX

KW Human; multispecific multivalent molecule; anti-Fc receptor; cytostatic;

KW anti-enhancement factor protein; breast; ovarian cancer; systemic lupus;

KW autoimmune disease; toxoplasma gondii; fungal infection; dermatological;

KW Fcgamma RI antibody hinge region; immunosuppressive; antimicrobial;

KW therapy.

XX

OS Homo sapiens.

XX

PN US2002032312-A1.

XX

PD 14-MAR-2002.

XX

PF 07-JUN-1995; 95US-00484172.

XX

PR 07-JUN-1995; 95US-00484172.

XX

PA (MEDA-) MEDAREX INC.

XX

PI Deo YM, Goldstein J, Graziano R, Somasundaram C;
 XX
 DR WPI; 1997-052242/05.
 DR N-PSDB; AAD35553.
 XX
 PT Recombinant, multi-specific anti-Fc receptor antibody molecules - also
 PT comprise an anti-target portion, used for the treatment of cancer,
 PT autoimmune disease and pathogenic infection.
 XX
 PS Example 2; Fig 1; 34pp; English.
 XX
 CC The invention relates to new multispecific multivalent molecules which
 CC comprise: a recombinant multispecific molecule comprising an anti-Fc
 CC receptor portion and an anti-target portion; a multivalent molecule
 CC comprising at least one anti-Fc receptor portion and at least one anti-
 CC target portion; or a multispecific molecule having one anti-FcR, one anti-
 CC -target portion and one anti-enhancement factor protein. The
 CC multispecific, multivalent molecules are useful for treating cancer or
 CC autoimmune disease, or for removing unwanted pathogens. These diseases
 CC include breast or ovarian cancer, toxoplasma gondii, fungal infection or
 CC systemic lupus. The present sequence is human Fcgamma RI antibody (H22)
 CC hinge region fragment
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 5 SSL 7

RESULT 69

AAW11502

ID AAW11502 standard; peptide; 11 AA.

XX

AC AAW11502;

XX

DT 24-SEP-1997 (first entry)

XX

DE Humanised anti-Fc gamma RI monoclonal antibody modified H-chain hinge.

XX

KW Humanised antibody; anti-Fc receptor; H22; bifunctional; bispecific;

KW fusion protein; chimera; breast cancer; ovarian cancer; HER2/neu;

KW small cell lung carcinoma; HIV; human immunodeficiency virus;

KW Toxoplasma gondii; candidiasis; autoimmune disease; vaccine;

KW immune thrombocytopenia purpura; systemic lupus erythematosus;

KW heavy chain.

XX

OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

OS Chimeric.

XX

FH Key Location/Qualifiers

FT Region 5. .11
FT /note= "New C-terminus; encoded by inserted sequence
FT which introduces XhoI and NotI restriction sites upstream
FT of a stop codon and a BamHI site downstream of the stop
FT codon"

XX

PN WO9640789-A1.

XX

PD 19-DEC-1996.

XX

PF 07-JUN-1996; 96WO-US009988.

XX

PR 07-JUN-1995; 95US-00484172.

XX

PA (MEDA-) MEDAREX INC.

XX

PI Deo YM, Goldstein J, Graziano R, Somasundaram C;

XX

DR WPI; 1997-052242/05.

DR N-PSDB; AAT58126.

XX

PT Recombinant, multi-specific anti-Fc receptor antibody molecules - also
PT comprise an anti-target portion, used for the treatment of cancer,
PT autoimmune disease and pathogenic infection.

XX

PS Example 2; Fig 1C; 115pp; English.

XX

CC New multispecific polypeptides comprise one portion that specifically
CC binds to Fc-gamma receptor 1 (Fc gamma RI), one portion that binds
CC specifically to one epitope of a target antigen and one portion that
CC binds specifically to a different site on the same target cell. The
CC multispecific molecules can be used to treat a number of diseases and
CC conditions dependent upon the identity of their anti-target portion. In
CC particular, they can be targetted against cancers (e.g. breast cancer,
CC ovarian cancer expressing HER2/neu, small cell carcinoma of the lung),
CC pathogenic infection (e.g. viral (HIV), protozoan (Toxoplasma gondii),
CC fungal (candidiasis)), and autoimmune disease (e.g. immune
CC thrombocytopenia purpura and systemic lupus erythematosus). They are also
CC useful for removing unwanted pathogens and in vaccines. In specific
CC examples, a humanised version of a mouse anti-Fc gamma RI monoclonal
CC antibody, designated H22, was used as part of a multispecific fusion
CC construct. To produce suitable fusion genes, the heavy chain of H22 had
CC to be modified; the CH2 and CH3 domains were removed and replaced by
CC ~~ligand coding sequences. PCR was used to engineer the sequence coding for~~
CC the new C-terminus of the heavy chain fragment having the present
CC sequence

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10

|||

Db 5 SSL 7

RESULT 70

AAW44188

ID AAW44188 standard; peptide; 11 AA.

XX

AC AAW44188;

XX

DT 12-MAY-1998 (first entry)

XX

DE H-2Kd-restricted cytotoxic T cell epitope HA2.

XX

KW H-2Kd-restricted cytotoxic T cell; CTL; epitope; nuclear protein;

KW influenza haemagglutinin; protection; influenza virus; immunisation.

XX

OS Synthetic.

OS Influenza virus.

XX

PN WO9741891-A1.

XX

PD 13-NOV-1997.

XX

PF 02-MAY-1997; 97WO-CA000296.

XX

PR 03-MAY-1996; 96CA-02175719.

XX

PA (CONN-) CONNAUGHT LAB LTD.

XX

PI Burt D, Sambhara S, Underdown B, Morein B, Klein MH;

XX

DR WPI; 1997-558696/51.

XX

PT Protecting against disease caused by influenza virus infection - by
PT immunising with solubilised influenza virus comprising haemagglutinin and
PT an immunostimulating complex also gives cross-protection.

XX

PS Example 4; Page 13; 39pp; English.

XX

CC A new method has been developed of protecting a host against disease
CC caused by infection with an influenza virus. The method comprises
CC administering a complex of solubilized influenza virus comprising
CC haemagglutinin (HA) (or fragment(s)) and an immunostimulating complex
CC (ISCOM) (flu-ISCOMs) to produce cytotoxic T cells specific for influenza
CC virus HA of H1 HA and H2 HA subtypes. A second method has been developed
CC which comprises administering substantially purified HA (or fragment(s))
CC retaining the immunological properties of HA incorporated into ISCOMs.
CC The present sequence represents a peptide used in an example of the
CC present invention. N.B. ISCOMs are known adjuvanted particulate vaccine
CC systems comprising cholesterol, phospholipid, antigen and Quil A (a
CC purified mixture of saponins from Quillaja saponaria). The methods can be
CC used to manufacture medicines (including vaccines) to stimulate cytotoxic
CC T cells specific for HA of both H1 HA and H2 HA subtypes of influenza
CC virus in a host, so protecting the host against disease caused by these
CC subtypes

XX

SQ Sequence 11 AA;

Query Match

27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 7 SSL 9

RESULT 71

AAW11511

ID AAW11511 standard; peptide; 11 AA.

XX

AC AAW11511;

XX

DT 24-SEP-1997 (first entry)

XX

DE Humanised anti-Fc gamma RI monoclonal antibody modified H-chain hinge.

XX

KW Humanised antibody; anti-Fc receptor; H22; bifunctional; bispecific;

KW fusion protein; chimera; immunoglobulin E; IgE; allergen; allergy;

KW Fc epsilon; heavy chain.

XX

OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

OS Chimeric.

XX

FH Key Location/Qualifiers

FT Region 5. .11

FT /note= "New C-terminus; encoded by inserted sequence

FT which introduces XhoI and NotI restriction sites upstream

FT of a stop codon and a BamHI site downstream of the stop

FT codon"

XX

PN W09640788-A1.

XX

PD 19-DEC-1996.

XX

PF 05-JUN-1996; 96WO-US009071.

XX

PR 07-JUN-1995; 95US-00479902.

XX

PA (MEDA-) MEDAREX INC.

XX

PI Guyre PM, Fanger M;

XX

DR WPI; 1997-052241/05.

DR N-PSDB; AAT58133.

XX

PT New bi-specific mol. with anti-effector cell and anti-IgE portions -

PT useful for preventing allergic reactions by reducing IgE antibody prodn.

PT and increasing IgG prodn.

XX

PS Example 1; Fig 1C; 18pp; English.

XX

CC New bispecific polypeptides comprise an anti-effector cell portion and an

CC anti-immunoglobulin E portion. In a specific example, a bispecific

CC protein was constructed by fusing a humanised version of a mouse anti-Fc
CC gamma RI monoclonal antibody, designated H22, and an IgE receptor. The
CC resulting polypeptide was able to bind to circulating IgE or to allergen
CC bound to IgE. To produce a suitable fusion gene, the heavy chain of H22
CC had to be modified; the CH2 and CH3 domains were removed and replaced by
CC ligand coding sequences. PCR was used to engineer the sequence coding for
CC the new C-terminus of the heavy chain fragment having the present
CC sequence
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
| | |
Db 5 SSL 7

RESULT 72

AAW30194

ID AAW30194 standard; peptide; 11 AA.

XX

AC AAW30194;

XX

DT 15-APR-1998 (first entry)

XX

DE Salvage receptor binding epitope.

XX

KW Salvage receptor binding epitope; antibody; ErbB3 protein; heregulin;
KW HRG; ErbB2-ErbB3 complex; inhibitor; tumour detection; therapy; lymphoma;
KW leukaemia; blastoma; carcinoma; sarcoma; inflammatory disorder;
KW angiogenic disease; immunological disease.

XX

OS Mammalia.

XX

PN WO9735885-A1.

XX

PD 02-OCT-1997.

XX

PF 07-MAR-1997; 97WO-US003546.

XX

PR 27-MAR-1996; 96US-00624036.

XX

PA (GETH) GENENTECH INC.

XX

PI Akita R, Sliwkowski M;

XX

DR WPI; 1997-489570/45.

XX

PT Antibody that binds to the ErbB3 receptor - used for diagnosis and
PT treatment of tumours, inflammation, angiogenesis and immunological
PT disease.

XX

PS Disclosure; Page 19; 44pp; English.

XX

CC This sequence represents a salvage receptor binding epitope that can be
 CC used in the antibody (AB) of the invention. The Ab of the invention is an
 CC Ab that binds to ErbB3 protein and reduces heregulin (HRG)-induced
 CC formation of an ErbB2-ErbB3 complex in cells producing both these
 CC proteins. The Ab are used for in vivo and in vitro detection of ErbB3 in
 CC binding assays, particularly for detection of tumours characterised by
 CC elevated ErbB3 expression. The Ab are also used for treatment and
 CC prevention of diseases associated with excessive activation of the ErbB2-
 CC ErbB3 complex, particularly benign or malignant tumours (e.g. leukaemia,
 CC lymphoma, blastoma, carcinoma or sarcoma), but also inflammation,
 CC angiogenic and immunological diseases. Also, the Ab can be used as
 CC affinity purification reagents

XX

SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9

|||

Db 3 NSS 5

RESULT 73

AAW15672

ID AAW15672 standard; peptide; 11 AA.

XX

AC AAW15672;

XX

DT 25-MAR-2003 (revised)

DT 11-JUN-1997 (first entry)

XX

DE Platelet aggregation inhibitor #97.

XX

KW Platelet aggregation inhibitor; RGD analogue; cyclic peptide; fibrinogen;

KW hydrophobically enhanced analogue; blood platelet; endothelial surface;

KW blood vessel; serum protein; GP IIb/IIIa glycoprotein complex; integrin;

KW plasma membrane; thrombosis; cell adhesion receptor; fibronectin;

KW vitronectin receptor; vascular graft occlusion; therapy.

XX

OS Synthetic.

XX

Key	Location/Qualifiers
FT Modified-site	1: .10
FT	/note= "forms peptide bond to create cyclic peptide"
XX	
PN	US5612311-A.
XX	
PD	18-MAR-1997.
XX	
PF	22-DEC-1994; 94US-00363963.
XX	
PR	06-APR-1990; 90US-00506444.
PR	05-APR-1991; 91US-00681119.
PR	14-APR-1993; 93US-00050736.
PR	02-MAR-1994; 94US-00204817.

XX
PA (LJOL-) LA JOLLA CANCER RES FOUND.
XX
PI Craig WS, Lukeman DS, Cheng S, Tschopp JF, Pierschbacher MD;
XX
DR WPI; 1997-192139/17.
XX
PT RGD-contg. peptide(s) that inhibit platelet aggregation - useful for
PT treating thrombosis.
XX
PS Example 5; Col 77; 50pp; English.
XX
CC AAW15576-W15695 represent platelet aggregation inhibitors. All of these
CC sequences are hydrophobically enhanced RGD peptide analogues. The
CC interaction of blood platelets with the endothelial surface of injured
CC blood vessels and with other platelets (platelet aggregation) is a major
CC factor in the course of development of thrombi. Thrombosis is a serious
CC condition which can cause tissue damage and eventually death (if
CC untreated). Platelet aggregation is dependent upon the binding of
CC fibrinogen and other serum proteins to the GP IIb/IIIa glycoprotein
CC complex on the platelet plasma membrane. GP IIb/IIIa is a member of the
CC integrin family of cell adhesion receptors, which are known to recognise
CC a RGD tripeptide recognition sequence. The peptides inhibit platelet
CC aggregation without prolonging bleeding time. These sequences have high
CC affinity for the IIb/IIIa receptor and low affinity for the fibronectin
CC and vitronectin receptors. The peptides are used as platelet aggregation
CC inhibitors for treating thrombosis and vascular graft occlusion. (Updated
CC on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RKG 6
| | |
Db 1 RKG 3

RESULT 74

AAW25009

ID AAW25009 standard; peptide; 11 AA.

XX

AC AAW25009;

XX

DT 25-MAR-2003 (revised)

DT 07-OCT-1997 (first entry)

XX

DE Oncoimmunin lymphoid factor peptide used for antibody production.

XX

KW Oncoimmunin myeloid factor; lymphoid factor; OI-M; OI-L; antibody;
KW tumour; cancer diagnosis; neoplasia; monoclonal; prognosis; melanoma.

XX

OS Homo sapiens.

XX

PN US5635356-A.

XX
 PD 03-JUN-1997.
 XX
 PF 22-MAR-1994; 94US-00218023.
 XX
 PR 31-MAY-1991; 91US-00707136.
 PR 23-SEP-1991; 91US-00764695.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Komoriya A, Packard B;
 XX
 DR WPI; 1997-309823/28.
 XX
 PT Antibody to onco:immunin-myeloid factor - for detection of onco:immunin-
 PT myeloid factor especially in tumour cell.
 XX
 PS Example 15; Col 43-44; 49pp; English.
 XX
 CC AAW25003-W25009 are peptides derived from an oncoimmunin-lymphoid (OI-L)
 CC factor derived from a melanoma cell line. The peptides were used for
 CC immunisation to produce monoclonal antibodies specific for the OI-L
 CC factor. Antibodies specific for an oncoimmunin-myeloid (OI-M) factor were
 CC also produced. Antibodies specific for OI-M or OI-L factors are used for
 CC detecting the factors in a sample, to screen tumour cells for production
 CC of the factors and hence identify cells as being of tumour origin. The
 CC antibodies are also useful to determine serum OI-M and OI-L levels for
 CC tumour diagnosis or for prognosis evaluation after tumour therapy.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
 |||
 Db 8 NSS 10

RESULT 75

AAW28862

ID AAW28862-standard; peptide; 11-AA.

XX

AC AAW28862;

XX

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 21-NOV-1997 (first entry)

XX

DE HTLV-1a,c derived peptide 50, recognised by HLA-B35.

XX

KW Human adult leukaemia; vaccine; prevention; therapy; epitope;

KW human leukocyte antigen; HLA-B35; cytotoxic T lymphocyte; diagnosis.

XX

OS Human T-lymphotropic virus type 1.

OS Human adult leukaemia virus 1c.
 XX
 PN JP09188696-A.
 XX
 PD 22-JUL-1997.
 XX
 PF 29-OCT-1993; 96JP-00220326.
 XX
 PR 29-OCT-1993; 93JP-00294472.
 XX
 PA (NOKI/) NOKIHARA K.
 PA (TAKI/) TAKIGUCHI M.
 XX
 DR WPI; 1997-420580/39.
 XX
 PT Synthetic peptide derived from human T cell leukaemia virus - is able to
 PT bind to HLA-B35 and is useful in a vaccine for prevention or treatment of
 PT human adult leukaemia.
 XX
 PS Claim 10; Page 2; 14pp; Japanese.
 XX
 CC The present sequence corresponds to amino acids 97-107 of pol from human
 CC adult leukaemia virus HTLV-1a,c. The synthetic peptide having this
 CC sequence is shown in cytotoxic T cells by combining with HLA-B35 antigen.
 CC The peptide can be used in a preventive vaccine and a therapeutic agent
 CC for human adult leukaemia caused by human T cell leukaemia virus.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 27-AUG-2003 to
 CC correct OS field.)
 XX
 SQ Sequence 11 AA;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 5 SSL 7

Search completed: April 8, 2004, 15:40:12
 Job time : 45.3077 secs

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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:08 ; Search time 11.3077 Seconds
(without alignments)
50.221 Million cell updates/sec

Title: US-09-787-443A-21
Perfect score: 11
Sequence: 1 AKSRKGNSSLM 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8542

Minimum DB seq length: 11
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	4	36.4	11	4	US-09-381-546-48	Sequence 48, Appl
2	3	27.3	11	1	US-07-696-551B-10	Sequence 10, Appl
3	3	27.3	11	1	US-08-030-731A-20	Sequence 20, Appl
4	3	27.3	11	1	US-07-851-941-12	Sequence 12, Appl
5	3	27.3	11	1	US-08-167-336A-11	Sequence 11, Appl
6	3	27.3	11	1	US-08-269-441A-14	Sequence 14, Appl
7	3	27.3	11	1	US-08-185-448-5	Sequence 5, Appli
8	3	27.3	11	1	US-08-190-788A-280	Sequence 280, App
9	3	27.3	11	1	US-08-167-035-38	Sequence 38, Appl
10	3	27.3	11	1	US-08-179-481-44	Sequence 44, Appl
11	3	27.3	11	1	US-08-218-023-9	Sequence 9, Appli

12	3	27.3	11	1	US-08-372-952-8	Sequence 8, Appli
13	3	27.3	11	1	US-07-958-903A-5	Sequence 5, Appli
14	3	27.3	11	1	US-07-958-903A-9	Sequence 9, Appli
15	3	27.3	11	1	US-07-958-903A-10	Sequence 10, Appl
16	3	27.3	11	1	US-07-958-903A-29	Sequence 29, Appl
17	3	27.3	11	1	US-07-958-903A-49	Sequence 49, Appl
18	3	27.3	11	1	US-08-416-962-11	Sequence 11, Appl
19	3	27.3	11	1	US-08-445-745-119	Sequence 119, App
20	3	27.3	11	1	US-08-208-887A-38	Sequence 38, Appl
21	3	27.3	11	1	US-08-467-420A-9	Sequence 9, Appli
22	3	27.3	11	1	US-08-470-110A-9	Sequence 9, Appli
23	3	27.3	11	1	US-08-462-018-5	Sequence 5, Appli
24	3	27.3	11	1	US-08-462-018-9	Sequence 9, Appli
25	3	27.3	11	1	US-08-462-018-10	Sequence 10, Appl
26	3	27.3	11	1	US-08-462-018-29	Sequence 29, Appl
27	3	27.3	11	1	US-08-462-018-49	Sequence 49, Appl
28	3	27.3	11	1	US-08-596-864-9	Sequence 9, Appli
29	3	27.3	11	1	US-08-422-101-3	Sequence 3, Appli
30	3	27.3	11	1	US-08-589-011-11	Sequence 11, Appl
31	3	27.3	11	1	US-08-422-091-3	Sequence 3, Appli
32	3	27.3	11	1	US-08-040-548-43	Sequence 43, Appl
33	3	27.3	11	1	US-08-466-344-43	Sequence 43, Appl
34	3	27.3	11	1	US-08-823-245-5	Sequence 5, Appli
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36	3	27.3	11	1	US-08-823-245-10	Sequence 10, Appl
37	3	27.3	11	1	US-08-823-245-29	Sequence 29, Appl
38	3	27.3	11	1	US-08-823-245-49	Sequence 49, Appl
39	3	27.3	11	1	US-08-667-769A-9	Sequence 9, Appli
40	3	27.3	11	1	US-08-465-391A-280	Sequence 280, App
41	3	27.3	11	2	US-08-452-724A-44	Sequence 44, Appl
42	3	27.3	11	2	US-08-940-371-9	Sequence 9, Appli
43	3	27.3	11	2	US-08-948-762-11	Sequence 11, Appl
44	3	27.3	11	2	US-08-539-005-38	Sequence 38, Appl
45	3	27.3	11	2	US-08-464-538B-280	Sequence 280, App
46	3	27.3	11	2	US-08-540-412-120	Sequence 120, App
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48	3	27.3	11	2	US-08-540-412-184	Sequence 184, App
49	3	27.3	11	2	US-08-540-412-191	Sequence 191, App
50	3	27.3	11	2	US-08-422-092-3	Sequence 3, Appli
51	3	27.3	11	2	US-08-468-819-14	Sequence 14, Appl
52	3	27.3	11	2	US-08-559-524A-11	Sequence 11, Appl
53	3	27.3	11	2	US-08-637-759B-76	Sequence 76, Appl
54	3	27.3	11	2	US-08-463-076E-370	Sequence 370, App
55	3	27.3	11	2	US-08-788-800-8	Sequence 8, Appli
56	3	27.3	11	2	US-08-982-597A-6	Sequence 6, Appli
57	3	27.3	11	2	US-08-747-137-63	Sequence 63, Appl
58	3	27.3	11	2	US-08-989-667-9	Sequence 9, Appli
59	3	27.3	11	2	US-09-121-527-4	Sequence 4, Appli
60	3	27.3	11	2	US-08-350-260A-485	Sequence 485, App
61	3	27.3	11	2	US-08-827-009-1	Sequence 1, Appli
62	3	27.3	11	2	US-08-343-443B-68	Sequence 68, Appl
63	3	27.3	11	2	US-08-466-860-3	Sequence 3, Appli
64	3	27.3	11	2	US-08-466-860-6	Sequence 6, Appli
65	3	27.3	11	3	US-08-871-355A-76	Sequence 76, Appl
66	3	27.3	11	3	US-08-904-446A-6	Sequence 6, Appli
67	3	27.3	11	3	US-08-904-446A-7	Sequence 7, Appli
68	3	27.3	11	3	US-08-159-339A-1131	Sequence 1131, Ap

69	3	27.3	11	3	US-08-974-899-16	Sequence 16, Appl
70	3	27.3	11	3	US-08-749-707-11	Sequence 11, Appl
71	3	27.3	11	3	US-09-136-218-6	Sequence 6, Appli
72	3	27.3	11	3	US-08-472-040A-3	Sequence 3, Appli
73	3	27.3	11	3	US-08-472-040A-6	Sequence 6, Appli
74	3	27.3	11	3	US-08-817-177-4	Sequence 4, Appli
75	3	27.3	11	3	US-08-491-954-93	Sequence 93, Appl
76	3	27.3	11	3	US-08-422-093-3	Sequence 3, Appli
77	3	27.3	11	3	US-08-891-845-5	Sequence 5, Appli
78	3	27.3	11	3	US-08-422-112-3	Sequence 3, Appli
79	3	27.3	11	3	US-08-637-647-9	Sequence 9, Appli
80	3	27.3	11	3	US-09-051-342-120	Sequence 120, App
81	3	27.3	11	3	US-09-051-342-123	Sequence 123, App
82	3	27.3	11	3	US-09-051-342-184	Sequence 184, App
83	3	27.3	11	3	US-09-051-342-191	Sequence 191, App
84	3	27.3	11	3	US-08-855-958-4	Sequence 4, Appli
85	3	27.3	11	3	US-08-855-958-9	Sequence 9, Appli
86	3	27.3	11	3	US-08-468-161-120	Sequence 120, App
87	3	27.3	11	3	US-08-468-161-123	Sequence 123, App
88	3	27.3	11	3	US-09-097-171A-4	Sequence 4, Appli
89	3	27.3	11	3	US-09-051-759-120	Sequence 120, App
90	3	27.3	11	3	US-09-051-759-123	Sequence 123, App
91	3	27.3	11	3	US-09-051-759-184	Sequence 184, App
92	3	27.3	11	3	US-09-051-759-191	Sequence 191, App
93	3	27.3	11	3	US-08-875-309-8	Sequence 8, Appli
94	3	27.3	11	3	US-08-652-877-51	Sequence 51, Appl
95	3	27.3	11	3	US-08-276-776-3	Sequence 3, Appli
96	3	27.3	11	3	US-08-276-776-6	Sequence 6, Appli
97	3	27.3	11	3	US-08-471-209-3	Sequence 3, Appli
98	3	27.3	11	3	US-08-471-209-6	Sequence 6, Appli
99	3	27.3	11	3	US-08-861-423A-11	Sequence 11, Appl
100	3	27.3	11	3	US-09-177-249-286	Sequence 286, App

ALIGNMENTS

RESULT 1

US-09-381-546-48

; Sequence 48, Application US/09381546

; Patent No. 6451976

; GENERAL INFORMATION:

; APPLICANT: Trigen Limited

; TITLE OF INVENTION: BI- OR MULTIFUNCTIONAL MOLECULES BASED ON A DENDROASPIN

; TITLE OF INVENTION: SCAFFOLD

; FILE REFERENCE: P41007WO

; CURRENT APPLICATION NUMBER: US/09/381,546

; CURRENT FILING DATE: 1999-09-20

; PRIOR APPLICATION NUMBER: PCT/GB98/00848

; PRIOR FILING DATE: 1998-09-20

; PRIOR APPLICATION NUMBER: GB9705787.1

; PRIOR FILING DATE: 1997-03-20

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 48

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acids
; OTHER INFORMATION: encoded by bases 921-956 of pGEX-3X
US-09-381-546-48

Query Match 36.4%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GNSS 9
| | | |
Db 8 GNSS 11

RESULT 2

US-07-696-551B-10
; Sequence 10, Application US/07696551B
; Patent No. 5232841
; GENERAL INFORMATION:
; APPLICANT: Hashimoto, Tamotsu
; APPLICANT: Tsujimura, Atsushi
; APPLICANT: Udaka, Shigezo
; TITLE OF INVENTION: Process for Preparing Peptide
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS/PC-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/696,551B
; FILING DATE: 19910509
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-122166
; FILING DATE: 11-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-334575
; FILING DATE: 30-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence M. Lavin, Jr.
; REGISTRATION NUMBER: 30,768
; REFERENCE/DOCKET NUMBER: 2481-1070
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-696-551B-10

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GNS 8
| | |
Db 7 GNS 9

RESULT 3

US-08-030-731A-20

; Sequence 20, Application US/08030731A
; Patent No. 5426036
; GENERAL INFORMATION:
; APPLICANT: Koller, Klaus-Peter
; APPLICANT: Riess, Guenther Johannes
; APPLICANT: Uhlmann, Eugen
; APPLICANT: Wallmeier, Holger
; TITLE OF INVENTION: Processes for the Preparation of Foreign
; TITLE OF INVENTION: Proteins in Streptomyces
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/030,731A
; FILING DATE: 12-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/189,840
; FILING DATE: 03-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/430,622
; FILING DATE: 01-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/687,610
; FILING DATE: 19-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,757
; FILING DATE: 29-JUL-1991


```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 37 14 866.4
; FILING DATE: 05-MAY-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 38 37 273.8
; FILING DATE: 03-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 39 27 449.7
; FILING DATE: 19-AUG-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 12 818.0
; FILING DATE: 21-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Kirschner Michael K.
; REGISTRATION NUMBER: 34,851
; REFERENCE/DOCKET NUMBER: 02481-0593-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-030-731A-20

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      6 GNS 8
      |||
Db      7 GNS 9

```

RESULT 4

US-07-851-941-12

```

; Sequence 12, Application US/07851941
; Patent No. 5428016
; GENERAL INFORMATION:
; APPLICANT: Mamoru TOMITA et al.
; TITLE OF INVENTION: Antimicrobial Peptide and an
; TITLE OF INVENTION: Antimicrobial Agent
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: DisplayWrite

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/851,941
; FILING DATE: 19920313
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/851,941
; FILING DATE: March 13, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acid residues
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:

; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-851-941-12

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KSR 4
|||
Db 1 KSR 3

RESULT 5

US-08-167-336A-11

; Sequence 11, Application US/08167336A
; Patent No. 5531990
; GENERAL INFORMATION:
; APPLICANT: THANAVALA, YASMIN
; APPLICANT: THAKUR, ARVIND
; APPLICANT: ROITT, IVAN
; APPLICANT: PRIDE, MICHAEL
; TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODY
; TITLE OF INVENTION: HAVING CORRESPONDENCE WITH HUMAN HEPATITIS
; TITLE OF INVENTION: B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DUNN & ASSOCIATES, P.C.
; STREET: P.O. BOX 96
; CITY: NEWFANE
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 14108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; COMPUTER: VICTOR 300 SX/25
; OPERATING SYSTEM: MS-DOS VERSION 5.0
; SOFTWARE: WORDSTAR PROFESSIONAL RELEASE 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,336A
; FILING DATE: 15-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: DUNN, MICHAEL L.
; REGISTRATION NUMBER: 25,330
; REFERENCE/DOCKET NUMBER: RPP:138 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 433-1661
; TELEFAX: (716) 433-1665
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN

```

;      TOPOLOGY:   UNKNOWN
;      MOLECULE TYPE:  PEPTIDE
;      HYPOTHETICAL:
;      ANTI-SENSE:
;      FRAGMENT TYPE:
;      ORIGINAL SOURCE:
;      ORGANISM:
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:
;      CELL LINE:
;      ORGANELLE:
;      IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:
;      POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;      FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;      PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      DOCUMENT NUMBER:
;      FILING DATE:
;      PUBLICATION DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:
US-08-167-336A-11

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```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          6 GNS 8
            |||
Db          7 GNS 9

```

RESULT 6

US-08-269-441A-14

; Sequence 14, Application US/08269441A

; Patent No. 5552529

; GENERAL INFORMATION:

; APPLICANT: Rearden, Ann

; TITLE OF INVENTION: A NOVEL AUTOANTIGEN, PINCH

```

; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/269,441A
; FILING DATE: 30-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
US-08-269-441A-14

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```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 NSS 9
        |||
Db      3 NSS 5

```

RESULT 7

US-08-185-448-5

```

; Sequence 5, Application US/08185448
; Patent No. 5580747
; GENERAL INFORMATION:
; APPLICANT: SHULTZ, JOHN W.
; APPLICANT: WHITE, DOUGLAS H.
; TITLE OF INVENTION: NON-RADIOACTIVE KINASE,
; TITLE OF INVENTION: PHOSPHATASE AND PROTEASE ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ANDRUS, SCEALES, STARKE & SAWALL

```

```

; STREET: 100 E. WISCONSIN AVENUE, SUITE 1100
; CITY: MILWAUKEE
; STATE: WISCONSIN
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,448
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/791,928
; FILING DATE: 12-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SARA, CHARLES S
; REGISTRATION NUMBER: 30492
; REFERENCE/DOCKET NUMBER: F.3347-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 255-2022
; TELEFAX: (608) 255-2182
; TELEX: 26832 ANDSTARK
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Binding-site
; LOCATION: 1
; OTHER INFORMATION: /label= LABEL
; OTHER INFORMATION: /note= "LOCATION OF LISSAMINE RHODAMINE
; OTHER INFORMATION: DETECTION TAG"
US-08-185-448-5

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 KSR 4
      |||
Db      6 KSR 8

```

```

RESULT 8
US-08-190-788A-280
; Sequence 280, Application US/08190788A
; Patent No. 5608035
; GENERAL INFORMATION:
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Baldwin, David N.

```

; APPLICANT: Jacobs, Jeff W.
 ; TITLE OF INVENTION: Peptides and Compounds That Bind to the
 ; TITLE OF INVENTION: IL-1 Receptor
 ; NUMBER OF SEQUENCES: 312
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Affymax Technologies N.V.
 ; STREET: 4001 Miranda Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/190,788A
 ; FILING DATE: 02-FEB-1994
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/847,567
 ; FILING DATE: 05-MAR-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stevens, Lauren L.
 ; REGISTRATION NUMBER: 36,691
 ; REFERENCE/DOCKET NUMBER: 1019.1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-496-2300
 ; TELEFAX: 415-424-0832
 ; INFORMATION FOR SEQ ID NO: 280:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-190-788A-280

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
 |||
 Db 2 NSS 4

RESULT 9

US-08-167-035-38

; Sequence 38, Application US/08167035
 ; Patent No. 5618691

; GENERAL INFORMATION:

; APPLICANT: Schlessinger, Joseph
 ; APPLICANT: Skolnick, Edward Y.
 ; APPLICANT: Margolis, Benjamin L.
 ; TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR

```

; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE
; TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: 10036-2711
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,035
; FILING DATE: 16-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-167-035-38

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 NSS 9
      |||
Db      3 NSS 5

```

RESULT 10

```

US-08-179-481-44
; Sequence 44, Application US/08179481
; Patent No. 5624816
; GENERAL INFORMATION:
; APPLICANT: CARRAWAY, KERMIT L.
; APPLICANT: CAROTHERS CARRAWAY, CORALIE A.
; APPLICANT: FREGIEN, NEVIS L.
; TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
; NUMBER OF SEQUENCES: 125
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: 1100 NEW YORK AVENUE, N.W.

```


; CITY: WASHINGTON
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005-3918
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/179,481
 ; FILING DATE: 28-DEC-1993
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/922,521
 ; FILING DATE: 30-JUL-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KOKULIS, PAUL N.
 ; REGISTRATION NUMBER: 16,773
 ; REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 861-3000
 ; TELEFAX: (202) 822-0944
 ; TELEX: 6714627 CUSH
 ; INFORMATION FOR SEQ ID NO: 44:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-179-481-44

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 2 SSL 4

RESULT 11
 US-08-218-023-9
 ; Sequence 9, Application US/08218023
 ; Patent No. 5635356
 ; GENERAL INFORMATION:
 ; APPLICANT: Packard, Beverly
 ; APPLICANT: Komoriya, Akira
 ; TITLE OF INVENTION: ONCOIMMUNINS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend Khourie and Crew
 ; STREET: Steuart Street Tower, One Market Plaza
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: US

```

; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218,023
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 15280-132-1,E12691/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-218-023-9

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```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 NSS 9
      |||
Db      8 NSS 10

```

RESULT 12

US-08-372-952-8

```

; Sequence 8, Application US/08372952
; Patent No. 5645837
; GENERAL INFORMATION:
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Choksi, Swati
; APPLICANT: Korngold, Robert
; TITLE OF INVENTION: CD8 Antagonists
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 5645837ris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/372,952
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1440
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-372-952-8

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Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 NSS 9
        |||
Db      6 NSS 8

```

RESULT 13

US-07-958-903A-5

```

; Sequence 5, Application US/07958903A
; Patent No. 5652214
; GENERAL INFORMATION:
; APPLICANT: Lewis, Michael E.
; APPLICANT: Kauer, James C.
; APPLICANT: Smith, Kevin R.
; APPLICANT: Callison, Kathleen V.
; APPLICANT: Baldino, Frank
; APPLICANT: Neff, Nicola
; APPLICANT: Iqbal, Mohamed
; TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION
; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

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;   COMPUTER:  IBM PS/2 Model 50Z or 55SX
;   OPERATING SYSTEM:  MS-DOS (Version 5.0)
;   SOFTWARE:  WordPerfect (Version 5.1)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/07/958,903A
;     FILING DATE:  October 7, 1992
;     CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  07/361,595
;     FILING DATE:  June 5, 1989
;     APPLICATION NUMBER:  07/534,139
;     FILING DATE:  June 5, 1990
;     APPLICATION NUMBER:  07/869,913
;     FILING DATE:  April 15, 1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Clark, Paul T.
;     REGISTRATION NUMBER:  30,162
;     REFERENCE/DOCKET NUMBER:  02655/003004
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (617) 542-5070
;     TELEFAX:  (617) 542-8906
;     TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
US-07-958-903A-5

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      1 AKS 3
      |||
Db      8 AKS 10

```

RESULT 14

US-07-958-903A-9

```

; Sequence 9, Application US/07958903A
; Patent No. 5652214

```

; GENERAL INFORMATION:

```

;   APPLICANT:  Lewis, Michael E.
;   APPLICANT:  Kauer, James C.
;   APPLICANT:  Smith, Kevin R.
;   APPLICANT:  Callison, Kathleen V.
;   APPLICANT:  Baldino, Frank
;   APPLICANT:  Neff, Nicola
;   APPLICANT:  Iqbal, Mohamed
;   TITLE OF INVENTION:  TREATING DISORDERS BY APPLICATION
;   TITLE OF INVENTION:  OF INSULIN-LIKE GROWTH FACTORS AND
;   TITLE OF INVENTION:  ANALOGS
;   NUMBER OF SEQUENCES:  56
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Fish & Richardson

```

```

; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/958,903A
; FILING DATE: October 7, 1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/361,595
; FILING DATE: June 5, 1989
; APPLICATION NUMBER: 07/534,139
; FILING DATE: June 5, 1990
; APPLICATION NUMBER: 07/869,913
; FILING DATE: April 15, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 02655/003004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-07-958-903A-9

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AKS 3
      |||
Db      7 AKS 9

```

```

RESULT 15
US-07-958-903A-10
; Sequence 10, Application US/07958903A
; Patent No. 5652214
; GENERAL INFORMATION:
; APPLICANT: Lewis, Michael E.
; APPLICANT: Kauer, James C.
; APPLICANT: Smith, Kevin R.
; APPLICANT: Callison, Kathleen V.
; APPLICANT: Baldino, Frank
; APPLICANT: Neff, Nicola

```

```

; APPLICANT: Iqbal, Mohamed
; TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION
; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/958,903A
; FILING DATE: October 7, 1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/361,595
; FILING DATE: June 5, 1989
; APPLICATION NUMBER: 07/534,139
; FILING DATE: June 5, 1990
; APPLICATION NUMBER: 07/869,913
; FILING DATE: April 15, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 02655/003004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-07-958-903A-10

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 AKS 3
      |||
Db      7 AKS 9

```

```

RESULT 16
US-07-958-903A-29
; Sequence 29, Application US/07958903A
; Patent No. 5652214

```

```

; GENERAL INFORMATION:
; APPLICANT: Lewis, Michael E.
; APPLICANT: Kauer, James C.
; APPLICANT: Smith, Kevin R.
; APPLICANT: Callison, Kathleen V.
; APPLICANT: Baldino, Frank
; APPLICANT: Neff, Nicola
; APPLICANT: Iqbal, Mohamed
; TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION
; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/958,903A
; FILING DATE: October 7, 1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/361,595
; FILING DATE: June 5, 1989
; APPLICATION NUMBER: 07/534,139
; FILING DATE: June 5, 1990
; APPLICATION NUMBER: 07/869,913
; FILING DATE: April 15, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 02655/003004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-07-958-903A-29

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AKS 3
      |||

```

RESULT 17

US-07-958-903A-49

; Sequence 49, Application US/07958903A

; Patent No. 5652214

; GENERAL INFORMATION:

; APPLICANT: Lewis, Michael E.

; APPLICANT: Kauer, James C.

; APPLICANT: Smith, Kevin R.

; APPLICANT: Callison, Kathleen V.

; APPLICANT: Baldino, Frank

; APPLICANT: Neff, Nicola

; APPLICANT: Iqbal, Mohamed

; TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION

; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND

; TITLE OF INVENTION: ANALOGS

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 50Z or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/958,903A

; FILING DATE: October 7, 1992

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/361,595

; FILING DATE: June 5, 1989

; APPLICATION NUMBER: 07/534,139

; FILING DATE: June 5, 1990

; APPLICATION NUMBER: 07/869,913

; FILING DATE: April 15, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 02655/003004

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 49:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; FEATURE:

; OTHER INFORMATION: Xaa represents the D-isomer of tyrosine.
US-07-958-903A-49

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
|||
Db 7 AKS 9

RESULT 18

US-08-416-962-11

; Sequence 11, Application US/08416962

; Patent No. 5668253

; GENERAL INFORMATION:

; APPLICANT: THANAVALA, YASMIN

; APPLICANT: THAKUR, ARVIND

; APPLICANT: ROITT, IVAN

; APPLICANT: PRIDE, MICHAEL

; TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODY

; TITLE OF INVENTION: HAVING CORRESPONDENCE WITH HUMAN HEPATITIS

; TITLE OF INVENTION: B SURFACE ANTIGEN

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DUNN & ASSOCIATES, P.C.

; STREET: P.O. BOX 96

; CITY: NEWFANE

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 14108

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB

; COMPUTER: VICTOR 300 SX/25

; OPERATING SYSTEM: MS-DOS VERSION 5.0

; SOFTWARE: WORDSTAR PROFESSIONAL RELEASE 4

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/416,962

; FILING DATE: 05-APR-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/167,336

; FILING DATE: 15-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: DUNN, MICHAEL L.

; REGISTRATION NUMBER: 25,330

; REFERENCE/DOCKET NUMBER: RPP:138 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (716) 433-1661

; TELEFAX: (716) 433-1665

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11

; TYPE: AMINO ACID

; STRANDEDNESS: UNKNOWN

; TOPOLOGY: UNKNOWN

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; MOLECULE TYPE:  PEPTIDE
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
;   ORGANISM:
;   STRAIN:
;   INDIVIDUAL ISOLATE:
;   DEVELOPMENTAL STAGE:
;   HAPLOTYPE:
;   TISSUE TYPE:
;   CELL TYPE:
;   CELL LINE:
;   ORGANELLE:
; IMMEDIATE SOURCE:
;   LIBRARY:
;   CLONE:
; POSITION IN GENOME:
;   CHROMOSOME/SEGMENT:
;   MAP POSITION:
;   UNITS:
; FEATURE:
;   NAME/KEY:
;   LOCATION:
;   IDENTIFICATION METHOD:
;   OTHER INFORMATION:
; PUBLICATION INFORMATION:
;   AUTHORS:
;   TITLE:
;   JOURNAL:
;   VOLUME:
;   ISSUE:
;   PAGES:
;   DATE:
;   DOCUMENT NUMBER:
;   FILING DATE:
;   PUBLICATION DATE:
;   RELEVANT RESIDUES IN SEQ ID NO:
US-08-416-962-11

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.7e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy          6 GNS 8
            |||
Db          7 GNS 9

```

```

RESULT 19
US-08-445-745-119
; Sequence 119, Application US/08445745
; Patent No. 5672585
; GENERAL INFORMATION:
;   APPLICANT:  Pierschbacher, Michael D.
;   APPLICANT:  Cheng, Soan
;   APPLICANT:  Craig, William S.

```

```

; APPLICANT: Tschopp, Juerg F.
; TITLE OF INVENTION: Methods and Composition for Treating
; TITLE OF INVENTION: Thrombosis
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,745
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/171,068
; FILING DATE: 20-DEC-1993
; APPLICATION NUMBER: US 08/079,441
; FILING DATE: 18-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/050,73614
; FILING DATE: 14-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/681,119
; FILING DATE: 05-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/506,444
; FILING DATE: 06-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 9829
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-08-445-745-119

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      4 RKG 6
      |||
Db      1 RKG 3

```

RESULT 20

US-08-208-887A-38

; Sequence 38, Application US/08208887A

; Patent No. 5677421

; GENERAL INFORMATION:

; APPLICANT: Schlessinger, Joseph

; APPLICANT: Skolnick, Edward Y.

; APPLICANT: Margolis, Benjamin L.

; TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR

; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE

; TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PENNIE & EDMONDS

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: 10036-2711

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/208,887A

; FILING DATE: 11-MAR-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7683-063

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-208-887A-38

Query Match 27.3%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9

|||

Db 3 NSS 5

RESULT 21

US-08-467-420A-9

; Sequence 9, Application US/08467420A

; Patent No. 5683892

```

; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P. O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,420A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270-5024
; TELEFAX: 610 270-5090
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-467-420A-9

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 SSL 10
      |||
Db      4 SSL 6

```

RESULT 22
 US-08-470-110A-9
 ; Sequence 9, Application US/08470110A
 ; Patent No. 5693323
 ; GENERAL INFORMATION:
 ; APPLICANT: Ames, Robert S.
 ; APPLICANT: Appelbaum, Edward R.
 ; APPLICANT: Chaiken, Irwin M.
 ; APPLICANT: Cook, Richard M.
 ; APPLICANT: Gross, Mitchell S.
 ; APPLICANT: Holmes, Stephen D.
 ; APPLICANT: McMillan, Lynette J.
 ; APPLICANT: Theisen, Timothy W.
 ; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
 ; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
 ; NUMBER OF SEQUENCES: 74
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corp./Corporate
 ; ADDRESSEE: Intellectual Property
 ; STREET: P. O. Box 1539-UW2220
 ; CITY: King of Prussia
 ; STATE: Pennsylvania
 ; COUNTRY: USA
 ; ZIP: 19406-0939
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,110A
 ; FILING DATE:
 ; CLASSIFICATION: 426
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/363131
 ; FILING DATE: 23-DEC-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sutton, Jeffrey A.
 ; REGISTRATION NUMBER: 34,028
 ; REFERENCE/DOCKET NUMBER: P50282
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 610 270-5024
 ; TELEFAX: 610 270-5090
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-470-110A-9

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10

Db 111
 4 SSL 6

RESULT 23

US-08-462-018-5

; Sequence 5, Application US/08462018

; Patent No. 5703045

; GENERAL INFORMATION:

; APPLICANT: Lewis, Michael E.

; APPLICANT: Kauer, James C.

; APPLICANT: Smith, Kevin R.

; APPLICANT: Callison, Kathleen V.

; APPLICANT: Baldino, Frank

; APPLICANT: Neff, Nicola

; APPLICANT: Iqbal, Mohamed

; TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION

; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND

; TITLE OF INVENTION: ANALOGS

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 50Z or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,018

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/958,903

; FILING DATE: October 7, 1992

; APPLICATION NUMBER: 07/361,595

; FILING DATE: June 5, 1989

; APPLICATION NUMBER: 07/534,139

; FILING DATE: June 5, 1990

; APPLICATION NUMBER: 07/869,913

; FILING DATE: April 15, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 02655/003005

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11

; TYPE: amino acid

; STRANDEDNESS:
; TOPOLOGY: linear
US-08-462-018-5

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
|||
Db 8 AKS 10

RESULT 24

US-08-462-018-9

; Sequence 9, Application US/08462018
; Patent No. 5703045

; GENERAL INFORMATION:

; APPLICANT: Lewis, Michael E.
; APPLICANT: Kauer, James C.
; APPLICANT: Smith, Kevin R.
; APPLICANT: Callison, Kathleen V.
; APPLICANT: Baldino, Frank
; APPLICANT: Neff, Nicola
; APPLICANT: Iqbal, Mohamed
; TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION
; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,018
; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/958,903
; FILING DATE: October 7, 1992
; APPLICATION NUMBER: 07/361,595
; FILING DATE: June 5, 1989
; APPLICATION NUMBER: 07/534,139
; FILING DATE: June 5, 1990
; APPLICATION NUMBER: 07/869,913
; FILING DATE: April 15, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 02655/003005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-462-018-9

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
|||
Db 7 AKS 9

RESULT 25

US-08-462-018-10

; Sequence 10, Application US/08462018
; Patent No. 5703045

; GENERAL INFORMATION:

; APPLICANT: Lewis, Michael E.
; APPLICANT: Kauer, James C.
; APPLICANT: Smith, Kevin R.
; APPLICANT: Callison, Kathleen V.
; APPLICANT: Baldino, Frank
; APPLICANT: Neff, Nicola
; APPLICANT: Iqbal, Mohamed

; TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION
; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,018
; FILING DATE:
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/958,903
; FILING DATE: October 7, 1992

```

; APPLICATION NUMBER: 07/361,595
; FILING DATE: June 5, 1989
; APPLICATION NUMBER: 07/534,139
; FILING DATE: June 5, 1990
; APPLICATION NUMBER: 07/869,913
; FILING DATE: April 15, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 02655/003005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-462-018-10

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AKS 3
      |||
Db      7 AKS 9

```

RESULT 26

US-08-462-018-29

; Sequence 29, Application US/08462018

; Patent No. 5703045

; GENERAL INFORMATION:

; APPLICANT: Lewis, Michael E.

; APPLICANT: Kauer, James C.

; APPLICANT: Smith, Kevin R.

; APPLICANT: Callison, Kathleen V.

; APPLICANT: Baldino, Frank

; APPLICANT: Neff, Nicola

; APPLICANT: Iqbal, Mohamed

; TITLE OF INVENTION: TREATING DISORDERS BY APPLICATION

; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH FACTORS AND

; TITLE OF INVENTION: ANALOGS

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 50Z or 55SX

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;   OPERATING SYSTEM:  MS-DOS (Version 5.0)
;   SOFTWARE:  WordPerfect (Version 5.1)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/462,018
;   FILING DATE:
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  07/958,903
;   FILING DATE:  October 7, 1992
;   APPLICATION NUMBER:  07/361,595
;   FILING DATE:  June 5, 1989
;   APPLICATION NUMBER:  07/534,139
;   FILING DATE:  June 5, 1990
;   APPLICATION NUMBER:  07/869,913
;   FILING DATE:  April 15, 1992
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Clark, Paul T.
;   REGISTRATION NUMBER:  30,162
;   REFERENCE/DOCKET NUMBER:  02655/003005
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (617) 542-5070
;   TELEFAX:  (617) 542-8906
;   TELEX:  200154
;   INFORMATION FOR SEQ ID NO:  29:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11
;   TYPE:  amino acid
;   STRANDEDNESS:
;   TOPOLOGY:  linear
US-08-462-018-29

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.7e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      1 AKS 3
      |||
Db      7 AKS 9

```

RESULT 27

US-08-462-018-49

```

; Sequence 49, Application US/08462018
; Patent No. 5703045

```

GENERAL INFORMATION:

```

;   APPLICANT:  Lewis, Michael E.
;   APPLICANT:  Kauer, James C.
;   APPLICANT:  Smith, Kevin R.
;   APPLICANT:  Callison, Kathleen V.
;   APPLICANT:  Baldino, Frank
;   APPLICANT:  Neff, Nicola
;   APPLICANT:  Iqbal, Mohamed
;   TITLE OF INVENTION:  TREATING DISORDERS BY APPLICATION
;   TITLE OF INVENTION:  OF INSULIN-LIKE GROWTH FACTORS AND
;   TITLE OF INVENTION:  ANALOGS
;   NUMBER OF SEQUENCES:  56
;   CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: U.S.A.
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; COMPUTER: IBM PS/2 Model 50Z or 55SX
 ; OPERATING SYSTEM: MS-DOS (Version 5.0)
 ; SOFTWARE: WordPerfect (Version 5.1)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/462,018
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/958,903
 ; FILING DATE: October 7, 1992
 ; APPLICATION NUMBER: 07/361,595
 ; FILING DATE: June 5, 1989
 ; APPLICATION NUMBER: 07/534,139
 ; FILING DATE: June 5, 1990
 ; APPLICATION NUMBER: 07/869,913
 ; FILING DATE: April 15, 1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Clark, Paul T.
 ; REGISTRATION NUMBER: 30,162
 ; REFERENCE/DOCKET NUMBER: 02655/003005
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 542-5070
 ; TELEFAX: (617) 542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 49:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; FEATURE:
 ; OTHER INFORMATION: Xaa represents the D-isomer of tyrosine.
 US-08-462-018-49

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
 |||
 Db 7 AKS 9

RESULT 28
 US-08-596-864-9
 ; Sequence 9, Application US/08596864
 ; Patent No. 5731183
 ; GENERAL INFORMATION:
 ; APPLICANT: KOBAYASHI, KATSUNORI

; APPLICANT: YAMANAKA, SHIGERU
 ; APPLICANT: MIWA, KIYOSHI
 ; APPLICANT: SUZUKI, SHUNICHI
 ; APPLICANT: ETO, YUZURU
 ; APPLICANT: TANITA, YUKO
 ; APPLICANT: YOKOZEKI, KENZO
 ; APPLICANT: HASHIGUCHI, KENICHI
 ; TITLE OF INVENTION: BACILLUS-DERIVED TRANSGLUTAMINASE
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCCLELLEAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/596,864
 ; FILING DATE: 09-FEB-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 021963/1995
 ; FILING DATE: 09-FEB-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 226316/1995
 ; FILING DATE: 04-SEP-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: JP 013072/1996
 ; FILING DATE: 29-JAN-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 10-786-0
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-596-864-9

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
 |||

Db

6 NSS 8

RESULT 29

US-08-422-101-3

; Sequence 3, Application US/08422101
; Patent No. 5739277
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,101
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 932-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-422-101-3

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 3 NSS 5

RESULT 30

US-08-589-011-11
; Sequence 11, Application US/08589011
; Patent No. 5744135
; GENERAL INFORMATION:
; APPLICANT: THANAVALA, YASMIN
; APPLICANT: THAKUR, ARVIND
; APPLICANT: ROITT, IVAN
; APPLICANT: PRIDE, MICHAEL
; TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODY
; TITLE OF INVENTION: HAVING CORRESPONDENCE WITH HUMAN HEPATITIS
; TITLE OF INVENTION: B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DUNN & ASSOCIATES, P.C.
; STREET: P.O. BOX 96
; CITY: NEWFANE
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 14108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; COMPUTER: VICTOR 300 SX/25
; OPERATING SYSTEM: MS-DOS VERSION 5.0
; SOFTWARE: WORDSTAR PROFESSIONAL RELEASE 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,011
; FILING DATE: 19-JAN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/167,336
; FILING DATE: 15-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DUNN, MICHAEL L.
; REGISTRATION NUMBER: 25,330
; REFERENCE/DOCKET NUMBER: RPP:138 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 433-1661
; TELEFAX: (716) 433-1665
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE: PEPTIDE
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:

```

;   ORGANELLE:
;   IMMEDIATE SOURCE:
;   LIBRARY:
;   CLONE:
;   POSITION IN GENOME:
;   CHROMOSOME/SEGMENT:
;   MAP POSITION:
;   UNITS:
;   FEATURE:
;   NAME/KEY:
;   LOCATION:
;   IDENTIFICATION METHOD:
;   OTHER INFORMATION:
;   PUBLICATION INFORMATION:
;   AUTHORS:
;   TITLE:
;   JOURNAL:
;   VOLUME:
;   ISSUE:
;   PAGES:
;   DATE:
;   DOCUMENT NUMBER:
;   FILING DATE:
;   PUBLICATION DATE:
;   RELEVANT RESIDUES IN SEQ ID NO:
US-08-589-011-11

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Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

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Qy      6 GNS 8
      |||
Db      7 GNS 9

```

RESULT 31

US-08-422-091-3

```

; Sequence 3, Application US/08422091
; Patent No. 5747035
; GENERAL INFORMATION:
;   APPLICANT: Leonard Presta
;   APPLICANT: Brad Snedecor
;   TITLE OF INVENTION: Altered Polypeptides with Increased
;   TITLE OF INVENTION: Half-Life
;   NUMBER OF SEQUENCES: 31
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 460 Point San Bruno Blvd
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS

```



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;   SOFTWARE:  patin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/422,091
;   FILING DATE:  14-APR-1995
;   CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Lee, Wendy M.
;   REGISTRATION NUMBER:
;   REFERENCE/DOCKET NUMBER:  932-6
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415/225-1994
;   TELEFAX:  415/952-9881
;   TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
US-08-422-091-3

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.7e+03;
Matches      3;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      7 NSS 9
        |||
Db      3 NSS 5

```

RESULT 32

US-08-040-548-43

```

; Sequence 43, Application US/08040548
; Patent No. 5763209
; GENERAL INFORMATION:
;   APPLICANT:  Sukhatme, Vikas P.
;   TITLE OF INVENTION:  METHODS AND MATERIALS RELATING TO THE
;   TITLE OF INVENTION:  FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
;   NUMBER OF SEQUENCES:  67
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Arnold, White & Durkee
;   STREET:  321 No. 5763209th Clark Street, Suite 800
;   CITY:  Chicago
;   STATE:  Illinois
;   COUNTRY:  U.S.A.
;   ZIP:  60610
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/040,548
;   FILING DATE:
;   CLASSIFICATION:  514

```

; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coughlin, Daniel F.
 ; REGISTRATION NUMBER: 36,111
 ; REFERENCE/DOCKET NUMBER: arcd067
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 744-0090
 ; TELEFAX: (312) 245-4961
 ; INFORMATION FOR SEQ ID NO: 43:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-040-548-43

Query Match 27.3%; Score 3; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NSS 9
 |||
 Db 2 NSS 4

RESULT 33

US-08-466-344-43

; Sequence 43, Application US/08466344
 ; Patent No. 5773583

; GENERAL INFORMATION:

; APPLICANT: Sukhatme, Vikas P.
 ; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
 ; TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
 ; NUMBER OF SEQUENCES: 67
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: 321 No. 5773583th Clark Street, Suite 800
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60610

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/466,344
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/040,548
 ; FILING DATE: 31-MAR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Coughlin, Daniel F.
 ; REGISTRATION NUMBER: 36,111
 ; REFERENCE/DOCKET NUMBER: arcd067

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 744-0090
; TELEFAX: (312) 245-4961
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-466-344-43

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 2 NSS 4

RESULT 34

US-08-823-245-5

; Sequence 5, Application US/08823245
; Patent No. 5776897

; GENERAL INFORMATION:

; APPLICANT: Lewis, Michael
; APPLICANT: Kauer, James C.
; APPLICANT: Smith, Kevin R.
; APPLICANT: Callison, Kathleen V.
; APPLICANT: Baldino, Frank
; APPLICANT: Neff, Nicola
; APPLICANT: Iqbal, Mohamed
; TITLE OF INVENTION: TREATING DISORDERS BY
; TITLE OF INVENTION: APPLICATION
; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH
; TITLE OF INVENTION: FACTORS AND
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or
; COMPUTER: 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version
; SOFTWARE: 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,245
; FILING DATE: March 24, 1997
; CLASSIFICATION: 514

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/361,595
; FILING DATE: June 6, 1989
; APPLICATION NUMBER: 07/534,139
; FILING DATE: June 5, 1990
; APPLICATION NUMBER: 07/869,913
; FILING DATE: April 15, 1992
; APPLICATION NUMBER: 07/958,903
; FILING DATE: October 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Creeson, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: 02655/003008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
US-08-823-245-5

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Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AKS 3
        |||
Db      8 AKS 10

```

RESULT 35

US-08-823-245-9

```

; Sequence 9, Application US/08823245
; Patent No. 5776897
; GENERAL INFORMATION:
; APPLICANT: Lewis, Michael
; APPLICANT: Kauer, James C.
; APPLICANT: Smith, Kevin R.
; APPLICANT: Callison, Kathleen V.
; APPLICANT: Baldino, Frank
; APPLICANT: Neff, Nicola
; APPLICANT: Iqbal, Mohamed
; TITLE OF INVENTION: TREATING DISORDERS BY
; TITLE OF INVENTION: APPLICATION
; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH
; TITLE OF INVENTION: FACTORS AND
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts

```

```

; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or
; COMPUTER: 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version
; SOFTWARE: 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,245
; FILING DATE: March 24, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/361,595
; FILING DATE: June 6, 1989
; APPLICATION NUMBER: 07/534,139
; FILING DATE: June 5, 1990
; APPLICATION NUMBER: 07/869,913
; FILING DATE: April 15, 1992
; APPLICATION NUMBER: 07/958,903
; FILING DATE: October 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Creeson, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: 02655/003008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
US-08-823-245-9

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AKS 3
      |||
Db      7 AKS 9

```

```

RESULT 36
US-08-823-245-10
; Sequence 10, Application US/08823245
; Patent No. 5776897
; GENERAL INFORMATION:
; APPLICANT: Lewis, Michael
; APPLICANT: Kauer, James C.
; APPLICANT: Smith, Kevin R.
; APPLICANT: Callison, Kathleen V.
; APPLICANT: Baldino, Frank

```

```

; APPLICANT: Neff, Nicola
; APPLICANT: Iqbal, Mohamed
; TITLE OF INVENTION: TREATING DISORDERS BY
; TITLE OF INVENTION: APPLICATION
; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH
; TITLE OF INVENTION: FACTORS AND
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or
; COMPUTER: 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version
; SOFTWARE: 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,245
; FILING DATE: March 24, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/361,595
; FILING DATE: June 6, 1989
; APPLICATION NUMBER: 07/534,139
; FILING DATE: June 5, 1990
; APPLICATION NUMBER: 07/869,913
; FILING DATE: April 15, 1992
; APPLICATION NUMBER: 07/958,903
; FILING DATE: October 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Creeson, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: 02655/003008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
US-08-823-245-10

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 AKS 3
      |||

```

RESULT 37

US-08-823-245-29

; Sequence 29, Application US/08823245

; Patent No. 5776897

; GENERAL INFORMATION:

; APPLICANT: Lewis, Michael

; APPLICANT: Kauer, James C.

; APPLICANT: Smith, Kevin R.

; APPLICANT: Callison, Kathleen V.

; APPLICANT: Baldino, Frank

; APPLICANT: Neff, Nicola

; APPLICANT: Iqbal, Mohamed

; TITLE OF INVENTION: TREATING DISORDERS BY

; TITLE OF INVENTION: APPLICATION

; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH

; TITLE OF INVENTION: FACTORS AND

; TITLE OF INVENTION: ANALOGS

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 50Z or

; COMPUTER: 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version

; SOFTWARE: 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/823,245

; FILING DATE: March 24, 1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/361,595

; FILING DATE: June 6, 1989

; APPLICATION NUMBER: 07/534,139

; FILING DATE: June 5, 1990

; APPLICATION NUMBER: 07/869,913

; FILING DATE: April 15, 1992

; APPLICATION NUMBER: 07/958,903

; FILING DATE: October 7, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Creeson, Gary L.

; REGISTRATION NUMBER: 34,310

; REFERENCE/DOCKET NUMBER: 02655/003008

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 29:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
US-08-823-245-29

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
|||
Db 7 AKS 9

RESULT 38
US-08-823-245-49
; Sequence 49, Application US/08823245
; Patent No. 5776897
; GENERAL INFORMATION:
; APPLICANT: Lewis, Michael
; APPLICANT: Kauer, James C.
; APPLICANT: Smith, Kevin R.
; APPLICANT: Callison, Kathleen V.
; APPLICANT: Baldino, Frank
; APPLICANT: Neff, Nicola
; APPLICANT: Iqbal, Mohamed
; TITLE OF INVENTION: TREATING DISORDERS BY
; TITLE OF INVENTION: APPLICATION
; TITLE OF INVENTION: OF INSULIN-LIKE GROWTH
; TITLE OF INVENTION: FACTORS AND
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or
; COMPUTER: 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version
; SOFTWARE: 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,245
; FILING DATE: March 24, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/361,595
; FILING DATE: June 6, 1989
; APPLICATION NUMBER: 07/534,139
; FILING DATE: June 5, 1990


```

; APPLICATION NUMBER: 07/869,913
; FILING DATE: April 15, 1992
; APPLICATION NUMBER: 07/958,903
; FILING DATE: October 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Creeson, Gary L.
; REGISTRATION NUMBER: 34,310
; REFERENCE/DOCKET NUMBER: 02655/003008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; FEATURE:
; OTHER INFORMATION: Xaa represents the D-isomer of
; OTHER INFORMATION: tyrosine.
US-08-823-245-49

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 AKS 3
        |||
Db      7 AKS 9

```

RESULT 39

US-08-667-769A-9

```

; Sequence 9, Application US/08667769A
; Patent No. 5783184

```

GENERAL INFORMATION:

```

; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

```

;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/667,769A
;   FILING DATE:
;   CLASSIFICATION:  424
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US95/17082
;   FILING DATE:  22-DEC-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/470110
;   FILING DATE:  06-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/467420
;   FILING DATE:  06-JUN-1995
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/363131
;   FILING DATE:  23-DEC-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Sutton, Jeffrey A.
;   REGISTRATION NUMBER:  34,028
;   REFERENCE/DOCKET NUMBER:  P50503
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  610-270-5024
;   TELEFAX:  610-270-5090
;   INFORMATION FOR SEQ ID NO:  9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-667-769A-9

```

```

Query Match          27.3%;  Score 3;  DB 1;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      8 SSL 10
      |||
Db      4 SSL 6

```

```

RESULT 40
US-08-465-391A-280
; Sequence 280, Application US/08465391A
; Patent No. 5786331
;   GENERAL INFORMATION:
;   APPLICANT:  Barrett, Ronald W.
;   APPLICANT:  Yanofsky, Stephen D.
;   APPLICANT:  Baldwin, David
;   APPLICANT:  Jacobs, Jeff W.
;   APPLICANT:  Bovy, Phillipe R.
;   APPLICANT:  Leahy, Ellen M.
;   APPLICANT:  Pottorf, Richard S.
;   TITLE OF INVENTION:  Peptides and Compounds That Bind to the

```

```

; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 405
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,391A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,474
; FILING DATE: 01-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,788
; FILING DATE: 02-FEB-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5786331viel, Vern
; REGISTRATION NUMBER: 32,483
; REFERENCE/DOCKET NUMBER: 16528A-001840/1019.2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 280:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-465-391A-280

```

```

Query Match          27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 NSS 9
      |||
Db      2 NSS 4

```

```

RESULT 41
US-08-452-724A-44
; Sequence 44, Application US/08452724A
; Patent No. 5830650
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto

```

```

; TITLE OF INVENTION: Walk-Through Mutagenesis
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/452,724A
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,600
; FILING DATE: 05-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02362
; FILING DATE: 05-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/505,314
; FILING DATE: 05-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook Esq., David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: RC90-01AZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-452-724A-44

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      5 KGN 7
      |||
Db      5 KGN 7

```

```

RESULT 42
US-08-940-371-9
; Sequence 9, Application US/08940371
; Patent No. 5851525
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.

```

```

; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P. O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,371
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,110
; FILING DATE:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270-5024
; TELEFAX: 610 270-5090
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-940-371-9

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 SSL 10
        |||
Db      4 SSL 6

```

RESULT 43

US-08-948-762-11

; Sequence 11, Application US/08948762

; Patent No. 5856087

; GENERAL INFORMATION:

; APPLICANT: THANAVALA, YASMIN

; APPLICANT: THAKUR, ARVIND

; APPLICANT: ROITT, IVAN

; APPLICANT: PRIDE, MICHAEL

; TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODY

; TITLE OF INVENTION: HAVING CORRESPONDENCE WITH HUMAN HEPATITIS

; TITLE OF INVENTION: B SURFACE ANTIGEN

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DUNN & ASSOCIATES, P.C.

; STREET: P.O. BOX 96

; CITY: NEWFANE

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 14108

; COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB

; COMPUTER: VICTOR 300 SX/25

; OPERATING SYSTEM: MS-DOS VERSION 5.0

; SOFTWARE: WORDSTAR PROFESSIONAL RELEASE 4

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/948,762

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/589,011

; FILING DATE: 19-JAN-1996

; APPLICATION NUMBER: 08/167,336

; FILING DATE: 15-DEC-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: DUNN, MICHAEL L.

; REGISTRATION NUMBER: 25,330

; REFERENCE/DOCKET NUMBER: RPP:138 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (716) 433-1661

; TELEFAX: (716) 433-1665

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11

; TYPE: AMINO ACID

; STRANDEDNESS: UNKNOWN

; TOPOLOGY: UNKNOWN

; MOLECULE TYPE: PEPTIDE

; HYPOTHETICAL:

; ANTI-SENSE:

; FRAGMENT TYPE:

; ORIGINAL SOURCE:

; ORGANISM:

; STRAIN:

; INDIVIDUAL ISOLATE:

; DEVELOPMENTAL STAGE:

; HAPLOTYPE:

```

; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-948-762-11

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```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      6 GNS 8
      |||
Db      7 GNS 9

```

RESULT 44

US-08-539-005-38

```

; Sequence 38, Application US/08539005
; Patent No. 5858686

```

; GENERAL INFORMATION:

```

; APPLICANT: Schlessinger, Joseph
; APPLICANT: Skolnick, Edward Y.
; APPLICANT: Margolis, Benjamin L.
; TITLE OF INVENTION: NOVEL EXPRESSION CLONING METHOD FOR
; TITLE OF INVENTION: IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE
; TITLE OF INVENTION: KINASES AND NOVEL TARGET PROTEINS
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: 10036-2711

```

```

; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/539,005
; FILING DATE: 4-OCT-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/167,035
; FILING DATE: 16-DEC-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-539-005-38

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 NSS 9
      |||
Db      3 NSS 5

```

RESULT 45

US-08-464-538B-280

```

; Sequence 280, Application US/08464538B
; Patent No. 5861476

```

GENERAL INFORMATION:

```

; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; APPLICANT: Baldwin, David
; APPLICANT: Jacobs, Jeff W.
; APPLICANT: Bovy, Phillipe R.
; APPLICANT: Leahy, Ellen M.
; APPLICANT: Pottorf, Richard S.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 402
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor

```



```

;   CITY:  San Francisco
;   STATE:  California
;   COUNTRY:  USA
;   ZIP:  94111
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/464,538B
;   FILING DATE:  05-JUN-1995
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/373,474
;   FILING DATE:  01-FEB-1995
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 08/190,788
;   FILING DATE:  02-FEB-1994
;   CLASSIFICATION:  514
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Smith, William M.
;   REGISTRATION NUMBER:  30,223
;   REFERENCE/DOCKET NUMBER:  16528A-001810
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-326-2400
;   TELEFAX:  415-326-2422
;   INFORMATION FOR SEQ ID NO:  280:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-464-538B-280

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      7 NSS 9
      |||
Db      2 NSS 4

```

```

RESULT 46
US-08-540-412-120
; Sequence 120, Application US/08540412
; Patent No. 5866679
; GENERAL INFORMATION:
; APPLICANT:  DeFeo-Jones, Deborah
; APPLICANT:  Feng, Dong-Mei
; APPLICANT:  Garsky, Victor M.
; APPLICANT:  Jones, Raymond E.
; APPLICANT:  Oliff, Allen I.
; TITLE OF INVENTION:  NOVEL PEPTIDES

```

```

;   NUMBER OF SEQUENCES:  194
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  DAVID A. MUTHARD
;     STREET:    126 E. Lincoln Avenue, P.O. BOX 2000
;     CITY:     RAHWAY
;     STATE:    NEW JERSEY
;     COUNTRY:   U.S.A.
;     ZIP:      07065
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:    IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:    PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/540,412
;     FILING DATE:
;     CLASSIFICATION:    530
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Muthard, David A.
;     REGISTRATION NUMBER:  35,297
;     REFERENCE/DOCKET NUMBER:  19253IC
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (908)594-3903
;     TELEFAX:   (908)594-4720
;   INFORMATION FOR SEQ ID NO:  120:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 amino acids
;       TYPE:    amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:    NO
;     FRAGMENT TYPE:  internal
US-08-540-412-120

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      8 SSL 10
        |||
Db      9 SSL 11

```

RESULT 47

US-08-540-412-123

; Sequence 123, Application US/08540412

; Patent No. 5866679

; GENERAL INFORMATION:

; APPLICANT: DeFeo-Jones, Deborah

; APPLICANT: Feng, Dong-Mei

; APPLICANT: Garsky, Victor M.

; APPLICANT: Jones, Raymond E.

; APPLICANT: Oliff, Allen I.

; TITLE OF INVENTION: NOVEL PEPTIDES

; NUMBER OF SEQUENCES: 194

```

;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  DAVID A. MUTHARD
;   STREET:  126 E. Lincoln Avenue, P.O. BOX 2000
;   CITY:  RAHWAY
;   STATE:  NEW JERSEY
;   COUNTRY:  U.S.A.
;   ZIP:  07065
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/540,412
;   FILING DATE:
;   CLASSIFICATION:  530
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Muthard, David A.
;   REGISTRATION NUMBER:  35,297
;   REFERENCE/DOCKET NUMBER:  19253IC
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (908)594-3903
;   TELEFAX:  (908)594-4720
;   INFORMATION FOR SEQ ID NO:  123:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:  NO
;   FRAGMENT TYPE:  internal
US-08-540-412-123

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      8 SSL 10
      |||
Db      9 SSL 11

```

```

RESULT 48
US-08-540-412-184
; Sequence 184, Application US/08540412
; Patent No. 5866679
;   GENERAL INFORMATION:
;   APPLICANT:  DeFeo-Jones, Deborah
;   APPLICANT:  Feng, Dong-Mei
;   APPLICANT:  Garsky, Victor M.
;   APPLICANT:  Jones, Raymond E.
;   APPLICANT:  Oliff, Allen I.
;   TITLE OF INVENTION:  NOVEL PEPTIDES
;   NUMBER OF SEQUENCES:  194
;   CORRESPONDENCE ADDRESS:

```

```

;   ADDRESSEE:  DAVID A. MUTHARD
;   STREET:  126 E. Lincoln Avenue, P.O. BOX 2000
;   CITY:  RAHWAY
;   STATE:  NEW JERSEY
;   COUNTRY:  U.S.A.
;   ZIP:  07065
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/540,412
;   FILING DATE:
;   CLASSIFICATION:  530
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Muthard, David A.
;   REGISTRATION NUMBER:  35,297
;   REFERENCE/DOCKET NUMBER:  19253IC
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (908)594-3903
;   TELEFAX:  (908)594-4720
;   INFORMATION FOR SEQ ID NO:  184:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  11 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-540-412-184

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      8 SSL 10
      |||
Db      9 SSL 11

```

RESULT 49

US-08-540-412-191

; Sequence 191, Application US/08540412

; Patent No. 5866679

; GENERAL INFORMATION:

; APPLICANT: DeFeo-Jones, Deborah

; APPLICANT: Feng, Dong-Mei

; APPLICANT: Garsky, Victor M.

; APPLICANT: Jones, Raymond E.

; APPLICANT: Oliff, Allen I.

; TITLE OF INVENTION: NOVEL PEPTIDES

; NUMBER OF SEQUENCES: 194

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DAVID A. MUTHARD

; STREET: 126 E. Lincoln Avenue, P.O. BOX 2000

; CITY: RAHWAY

; STATE: NEW JERSEY

```

; COUNTRY: U.S.A.
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,412
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Muthard, David A.
; REGISTRATION NUMBER: 35,297
; REFERENCE/DOCKET NUMBER: 19253IC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3903
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 191:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-540-412-191

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 SSL 10
      |||
Db      9 SSL 11

```

RESULT 50

US-08-422-092-3

```

; Sequence 3, Application US/08422092
; Patent No. 5869046
; GENERAL INFORMATION:
; APPLICANT: Leonard Presta
; APPLICANT: Brad Snedecor
; TITLE OF INVENTION: Altered Polypeptides with Increased
; TITLE OF INVENTION: Half-Life
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

;   SOFTWARE:  patin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/422,092
;     FILING DATE:  14-APR-1995
;     CLASSIFICATION:  530
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Lee, Wendy M.
;     REGISTRATION NUMBER:
;     REFERENCE/DOCKET NUMBER:  932-4
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415/225-1994
;     TELEFAX:  415/952-9881
;     TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-422-092-3

```

```

Query Match          27.3%;  Score 3;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 2.7e+03;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      7 NSS 9
        |||
Db      3 NSS 5

```

RESULT 51

US-08-468-819-14

```

; Sequence 14, Application US/08468819
; Patent No. 5871723
;   GENERAL INFORMATION:
;     APPLICANT:  Strieter, Robert M.
;     APPLICANT:  Polverini, Peter J.
;     APPLICANT:  Kunkel, Steven L.
;     TITLE OF INVENTION:  CXC Chemokines as Regulators of
;     TITLE OF INVENTION:  Angiogenesis
;     NUMBER OF SEQUENCES:  93
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Arnold, White & Durkee
;       STREET:  P.O. Box 4433
;       CITY:  Houston
;       STATE:  TX
;       COUNTRY:  US
;       ZIP:  77210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/468,819

```

```

; FILING DATE: Concurrently herewith
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: UMIC:003/HYL
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-468-819-14

```

```

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      4 RKG 6
      |||
Db      5 RKG 7

```

RESULT 52

US-08-559-524A-11

```

; Sequence 11, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,524A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-00-US

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-559-524A-11

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 7 NSS 9

RESULT 53

US-08-637-759B-76

; Sequence 76, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,759B
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795

; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-76

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
|||
Db 6 AKS 8

RESULT 54

US-08-463-076E-370

; Sequence 370, Application US/08463076E
; Patent No. 5880096
; GENERAL INFORMATION:
; APPLICANT: Barrett, Ronald W.
; APPLICANT: Yanofsky, Stephen D.
; TITLE OF INVENTION: Peptides and Compounds That Bind to the
; TITLE OF INVENTION: IL-1 Receptor
; NUMBER OF SEQUENCES: 392
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,076E
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Snyder, Joseph R.
; REGISTRATION NUMBER: 39,381
; REFERENCE/DOCKET NUMBER: 16528A-001850US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 370:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-076E-370

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 2 NSS 4

RESULT 55

US-08-788-800-8

; Sequence 8, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-788-800-8

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 3 NSS 5

RESULT 56

US-08-982-597A-6

; Sequence 6, Application US/08982597A
; Patent No. 5932693
; GENERAL INFORMATION:
; APPLICANT: Santoro, Samuel A.
; APPLICANT: Staatz, William D.
; TITLE OF INVENTION: Antithrombotic Peptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer
; STREET: 800 No. 5932693th Lindbergh Blvd.
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,597A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/032,542
; FILING DATE: 10-DEC-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-3002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-3117
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-982-597A-6

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GNS 8
|||
Db 9 GNS 11

RESULT 57
 US-08-747-137-63
 ; Sequence 63, Application US/08747137
 ; Patent No. 5945033
 ; GENERAL INFORMATION:
 ; APPLICANT: YEN, Richard C.K.
 ; TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
 ; TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
 ; NUMBER OF SEQUENCES: 184
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, 8th Floor
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/747,137
 ; FILING DATE: 12-NOV-1996
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/212,546
 ; FILING DATE: 14-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/069,831
 ; FILING DATE: 01-JUN-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/959,560
 ; FILING DATE: 13-OCT-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/641,720
 ; FILING DATE: 15-JAN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Apple, Randolph T.
 ; REGISTRATION NUMBER: 36,429
 ; REFERENCE/DOCKET NUMBER: 016197-000840US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-576-0200
 ; INFORMATION FOR SEQ ID NO: 63:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: not relevant
 US-08-747-137-63

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KSR 4

Db III
 6 KSR 8

RESULT 58

US-08-989-667-9

; Sequence 9, Application US/08989667

; Patent No. 5948662

; GENERAL INFORMATION:

; APPLICANT: KOBAYASHI, KATSUNORI

; APPLICANT: YAMANAKA, SHIGERU

; APPLICANT: MIWA, KIYOSHI

; APPLICANT: SUZUKI, SHUNICHI

; APPLICANT: ETO, YUZURU

; APPLICANT: TANITA, YUKO

; APPLICANT: YOKOZEKI, KENZO

; APPLICANT: HASHIGUCHI, KENICHI

; TITLE OF INVENTION: BACILLUS-DERIVED TRANSGLUTAMINASE

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLEAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/989,667

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/596,864

; FILING DATE: 09-FEB-1996

; APPLICATION NUMBER: JP 021963/1995

; FILING DATE: 09-FEB-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 226316/1995

; FILING DATE: 04-SEP-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 013072/1996

; FILING DATE: 29-JAN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 10-786-0

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-989-667-9

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 6 NSS 8

RESULT 59

US-09-121-527-4
; Sequence 4, Application US/09121527
; Patent No. 5958775
; GENERAL INFORMATION:
; APPLICANT: WICKSTROM, ERIC
; APPLICANT: CLEAVER, STEPHEN
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR TARGETED INTEGRATION INTO
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: JEFF-0251
; CURRENT APPLICATION NUMBER: US/09/121,527
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 60/054,146
; EARLIER FILING DATE: 1997-07-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-121-527-4

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
|||
Db 5 AKS 7

RESULT 60

US-08-350-260A-485
; Sequence 485, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart

```

; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 485:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-350-260A-485

```

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 5 SRK 7

RESULT 61

US-08-827-009-1

; Sequence 1, Application US/08827009

; Patent No. 5968511

; GENERAL INFORMATION:

; APPLICANT: Akita, Robert

; APPLICANT: Sliwowski, Mark

; TITLE OF INVENTION: ErbB3 Antibodies

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/827,009

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/046850

; FILING DATE: 27-MAR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P1003R1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1994

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-827-009-1

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.7e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 3 NSS 5

RESULT 62

US-08-343-443B-68

; Sequence 68, Application US/08343443B

; Patent No. 5968734

; GENERAL INFORMATION:

; APPLICANT: Aurias, Alain

; APPLICANT: Delattre, Olivier

; APPLICANT: Desmaze, Chantal

; APPLICANT: Melot, Thomas

; APPLICANT: Peter, Martine

; APPLICANT: Ploougastel, Beatrice

; APPLICANT: Thomas, Gilles

; APPLICANT: Zucman, Jessica

; TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF

; TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL

; TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF

CANCEROUS

; TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM

SAID

; TITLE OF INVENTION: TRANSLOCATIONS

; NUMBER OF SEQUENCES: 129

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Weiser & Associates

; STREET: 230 South Fifteenth Street

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19102

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: AEDIT 1.0 DOS text editor

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/343,443B

; FILING DATE: 18-NOV-1994

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/FR93/00494

; FILING DATE: 19-MAY-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 92/06123

; FILING DATE: 20-MAY-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Weiser, Gerard J.

; REGISTRATION NUMBER: 19,763

; REFERENCE/DOCKET NUMBER: 989.6121P

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-875-8383

; TELEFAX: 215-875-8394

; INFORMATION FOR SEQ ID NO: 68:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-343-443B-68

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 SSL 10
|||
Db 6 SSL 8

RESULT 63

US-08-466-860-3

; Sequence 3, Application US/08466860
; Patent No. 5985552

; GENERAL INFORMATION:

; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; APPLICANT: CARLO, DENNIS J.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; TITLE OF INVENTION: POPULATIONS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/466,860
; FILING DATE:
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/813,867
; FILING DATE: 24-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 9107

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal

US-08-466-860-3

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 2 SSL 4

RESULT 64

US-08-466-860-6

; Sequence 6, Application US/08466860
; Patent No. 5985552
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; APPLICANT: CARLO, DENNIS J.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; TITLE OF INVENTION: POPULATIONS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,860
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,867
; FILING DATE: 24-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 9107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-466-860-6

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 2 SSL 4

RESULT 65

US-08-871-355A-76

; Sequence 76, Application US/08871355A
; Patent No. 6015669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/871,355A
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-76

Query Match 27.3%; Score 3; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3
|||
Db 6 AKS 8

RESULT 66

US-08-904-446A-6

; Sequence 6, Application US/08904446A

; Patent No. 6029114

; GENERAL INFORMATION:

; APPLICANT: Shamovsky, Igor L.

; APPLICANT: Ross, Gregory M.

; APPLICANT: Riopelle, Richard J.

; APPLICANT: Weaver, Donald F.

; TITLE OF INVENTION: Molecular Modelling of Neurotrophin-Receptor

; TITLE OF INVENTION: Binding

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dowell & Dowell, P.C.

; STREET: 1215 Jefferson Davis Highway, Suite 309

; CITY: Arlington

; STATE: Virginia

; COUNTRY: United States of America

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/904,446A

; FILING DATE: 31-JUL-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9616105.4

; FILING DATE: 31-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: RALPH A. DOWELL

; REGISTRATION NUMBER: 26868

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 415-2555

; TELEFAX: (703) 415-2559

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Peptide

; LOCATION: 1..11

; OTHER INFORMATION: /note= "C-terminal residues 108-118

; OTHER INFORMATION: of human NGF"

US-08-904-446A-6

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 6 SRK 8

RESULT 67

US-08-904-446A-7

; Sequence 7, Application US/08904446A
; Patent No. 6029114

; GENERAL INFORMATION:

; APPLICANT: Shamovsky, Igor L.
; APPLICANT: Ross, Gregory M.
; APPLICANT: Riopelle, Richard J.
; APPLICANT: Weaver, Donald F.
; TITLE OF INVENTION: Molecular Modelling of Neurotrophin-Receptor
; TITLE OF INVENTION: Binding
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dowell & Dowell, P.C.
; STREET: 1215 Jefferson Davis Highway, Suite 309
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/904,446A
; FILING DATE: 31-JUL-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9616105.4
; FILING DATE: 31-JUL-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: RALPH A. DOWELL
; REGISTRATION NUMBER: 26868

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 415-2555
; TELEFAX: (703) 415-2559

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "C-terminal residues 108-118"

; OTHER INFORMATION: of mouse NGF"
US-08-904-446A-7

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 6 SRK 8

RESULT 68

US-08-159-339A-1131

; Sequence 1131, Application US/08159339A
; Patent No. 6037135

; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:

; INFORMATION FOR SEQ ID NO: 1131:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1131

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 9 SRK 11

RESULT 69

US-08-974-899-16

; Sequence 16, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-974-899-16

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 3 NSS 5

RESULT 70

US-08-749-707-11

; Sequence 11, Application US/08749707
; Patent No. 6063582
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000
; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-749-707-11

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||

Db 7 NSS 9

RESULT 71

US-09-136-218-6

; Sequence 6, Application US/09136218
; Patent No. 6083914
; GENERAL INFORMATION:
; APPLICANT: Santoro, Samuel A.
; APPLICANT: Staatz, William D.
; TITLE OF INVENTION: Antithrombotic Peptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer
; STREET: 800 No. 6083914th Lindbergh Blvd.
; CITY: St. Louis
; STATE: MO
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/136,218
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/982,597
; FILING DATE:
; APPLICATION NUMBER: 60/032,542
; FILING DATE: 10-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: WU-3002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-694-3117
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-136-218-6

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GNS 8
|||
Db 9 GNS 11

RESULT 72

US-08-472-040A-3

; Sequence 3, Application US/08472040A
; Patent No. 6090387
; GENERAL INFORMATION:
; APPLICANT: HOWELL, MARK D.
; APPLICANT: BROSTOFF, STEVEN W.
; APPLICANT: CARLO, DENNIS J.
; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
; TITLE OF INVENTION: POPULATIONS
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES LLP
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,040A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IM 1641
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-08-472-040A-3

Query Match 27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 2 SSL 4

RESULT 73

US-08-472-040A-6

; Sequence 6, Application US/08472040A
; Patent No. 6090387
; GENERAL INFORMATION:

; APPLICANT: HOWELL, MARK D.
 ; APPLICANT: BROSTOFF, STEVEN W.
 ; APPLICANT: CARLO, DENNIS J.
 ; TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
 ; TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
 ; TITLE OF INVENTION: POPULATIONS
 ; NUMBER OF SEQUENCES: 77
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CAMPBELL & FLORES LLP
 ; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
 ; CITY: SAN DIEGO
 ; STATE: CALIFORNIA
 ; COUNTRY: UNITED STATES
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/472,040A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CAMPBELL, CATHRYN
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-IM 1641
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-535-9001
 ; TELEFAX: 619-535-8949
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: N-terminal
 US-08-472-040A-6

Query Match 27.3%; Score 3; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 2 SSL 4

RESULT 74
 US-08-817-177-4
 ; Sequence 4, Application US/08817177
 ; Patent No. 6096314
 ; GENERAL INFORMATION:
 ; APPLICANT: COHEN, Irun R.
 ; APPLICANT: ELIAS, Dana
 ; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
 ; TITLE OF INVENTION: COMPRISING THEM

```

; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark, P.L.L.C.
; STREET: 419 Seventh Street, N. W.
; CITY: Washington
; COUNTRY: US
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,177
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/12686
; FILING DATE: 10-OCTOBER-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: ISRAEL APP. NO. 111,196
; FILING DATE: 07-OCTOBER-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: COHEN=27
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-817-177-4

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Query Match          27.3%; Score 3; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

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Qy      8 SSL 10
      |||
Db      2 SSL 4

```

RESULT 75

US-08-491-954-93

; Sequence 93, Application US/08491954

; Patent No. 6096321

; GENERAL INFORMATION:

; APPLICANT: Girardeau, Jean-Pierre

; APPLICANT: Martin, Christine

; APPLICANT: Mechin, Marie-Claire

; APPLICANT: Der Vartanian, Maurice

; APPLICANT: Bousquet, Francois

; TITLE OF INVENTION: SUB-UNIT OF CS31A PROTEIN CAPSULE
 ; TITLE OF INVENTION: MODIFIED BY AT LEAST ONE HETEROLOGOUS PEPTIDE, CS31A
 ; TITLE OF INVENTION: PROTEIN CAPSULE INCLUDING SUCH A SUB-UNIT, AND
 ; TITLE OF INVENTION: MICROORGANISMS WHOSE OUTER MEMBRANE CARRIES SUCH
 ; TITLE OF INVENTION: SUB-UNITS, AND PROCEDURE FOR OBTAINING AND UTILIZING
 SUCH
 ; TITLE OF INVENTION: SUB-UNITS
 ; NUMBER OF SEQUENCES: 115
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WEISER & ASSOCIATES
 ; STREET: 230 South Fifteenth Street, Suite 500
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/491,954
 ; FILING DATE: 16-FEB-1996
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/FR93/01281
 ; FILING DATE: 21-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weiser, Gerard J.
 ; REGISTRATION NUMBER: 19,763
 ; REFERENCE/DOCKET NUMBER: 989.6264P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-875-8383
 ; TELEFAX: 215-875-8394
 ; INFORMATION FOR SEQ ID NO: 93:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-491-954-93

Query Match 27.3%; Score 3; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
 |||
 Db 1 NSS 3

Search completed: April 8, 2004, 15:52:16
 Job time : 12.3077 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 8.61538 Seconds
 (without alignments)
 122.816 Million cell updates/sec

Title: US-09-787-443A-21
 Perfect score: 11
 Sequence: 1 AKSRKGNSSLM 11

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 226

Minimum DB seq length: 11
 Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : PIR_78:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3	27.3	11	2	S66606	quinoline 2-oxidor
2	3	27.3	11	2	H54346	pyruvate synthase
3	3	27.3	11	2	G61497	seed protein ws-23
4	2	18.2	11	1	ECLQ2M	tachykinin II - mi
5	2	18.2	11	1	SPHO	substance P - hors
6	2	18.2	11	1	EOOCC	eledoisin - curled
7	2	18.2	11	1	A60654	substance P - guin
8	2	18.2	11	1	EOOC	eledoisin - musky
9	2	18.2	11	2	A33917	dihydroorotase (EC
10	2	18.2	11	2	JN0023	substance P - chic
11	2	18.2	11	2	A40693	transgelin - sheep
12	2	18.2	11	2	A38841	rhodopsin homolog
13	2	18.2	11	2	S09074	cytochrome P450-4b

14	2	18.2	11	2	D60409	kassinin-like pept
15	2	18.2	11	2	F60409	substance P-like p
16	2	18.2	11	2	E60409	substance P-like p
17	2	18.2	11	2	B26744	megascalikinin -
18	2	18.2	11	2	S23308	substance P - rain
19	2	18.2	11	2	S23306	substance P - Atla
20	2	18.2	11	2	B60409	kassinin-like pept
21	2	18.2	11	2	C60409	kassinin-like pept
22	2	18.2	11	2	S07203	uperolein - frog (
23	2	18.2	11	2	S07201	physalaemin - frog
24	2	18.2	11	2	A61033	ranatachykinin A -
25	2	18.2	11	2	B43669	hypothetical prote
26	2	18.2	11	2	PC2372	58K heat shock pro
27	2	18.2	11	2	S19775	wound-induced prot
28	2	18.2	11	2	S71304	amine oxidase (cop
29	2	18.2	11	2	A34135	DNA-binding protei
30	2	18.2	11	2	A26120	6-phosphofructokin
31	2	18.2	11	2	A35594	buccalin - Califor
32	2	18.2	11	2	S69349	neuropeptide FFami
33	2	18.2	11	2	S05002	corazonin - Americ
34	2	18.2	11	2	S33300	probable substance
35	2	18.2	11	2	S43626	cytochrome-c oxida
36	2	18.2	11	2	D42965	talin - chicken (f
37	2	18.2	11	2	I65231	CCK-B gastrin rece
38	2	18.2	11	2	E57789	gallbladder stone
39	2	18.2	11	2	I52980	glucocerebrosidase
40	2	18.2	11	2	PT0273	Ig heavy chain CRD
41	2	18.2	11	2	PT0302	Ig heavy chain CRD
42	2	18.2	11	2	S13279	Ile-Ser-bradykinin
43	2	18.2	11	2	I54193	Rhesus blood group
44	2	18.2	11	2	S68649	spermadhesin AQN-3
45	2	18.2	11	2	S68637	acetylcholinestera
46	2	18.2	11	2	A33571	follistatin - bovi
47	2	18.2	11	2	S23926	major glycoprotein
48	2	18.2	11	2	A14454	6-phosphofructokin
49	2	18.2	11	2	A29806	acidic proline-ric
50	2	18.2	11	2	PH1375	T antigen variant
51	2	18.2	11	2	PH1376	T antigen variant
52	2	18.2	11	2	PT0217	T-cell receptor be
53	2	18.2	11	2	PT0218	T-cell receptor be
54	2	18.2	11	2	D41946	T-cell receptor ga
55	2	18.2	11	2	B41946	T-cell receptor ga
56	2	18.2	11	2	C38887	T-cell receptor ga
57	2	18.2	11	2	I41946	T-cell receptor ga
58	2	18.2	11	2	PD0441	translation elonga
59	2	18.2	11	2	I60434	68kDa neurofilamen
60	2	18.2	11	2	S65377	cytochrome-c oxida
61	2	18.2	11	2	PH0939	T-cell receptor be
62	2	18.2	11	2	PH0940	T-cell receptor be
63	2	18.2	11	2	PH0941	T-cell receptor be
64	2	18.2	11	2	PH0929	T-cell receptor be
65	2	18.2	11	2	PH0891	T-cell receptor be
66	2	18.2	11	2	PH0938	T-cell receptor be
67	2	18.2	11	2	PH0947	T-cell receptor be
68	2	18.2	11	2	PH0903	T-cell receptor be
69	2	18.2	11	2	PH0904	T-cell receptor be
70	2	18.2	11	2	PH0924	T-cell receptor be

71	2	18.2	11	2	PH0919	T-cell receptor be
72	2	18.2	11	2	PH0914	T-cell receptor be
73	2	18.2	11	2	PH0922	T-cell receptor be
74	2	18.2	11	2	PH0906	T-cell receptor be
75	2	18.2	11	2	A34243	H-hyosophorin - Ja
76	2	18.2	11	2	S60294	tubulin 2 beta-3 c
77	2	18.2	11	4	I52708	ELAV-like neuronal
78	2	18.2	11	4	S19015	hypothetical prote
79	1	9.1	11	1	XAVIBH	bradykinin-potenti
80	1	9.1	11	1	XASNBA	bradykinin-potenti
81	1	9.1	11	1	GMROL	leucosulfakinin -
82	1	9.1	11	1	LFTWWE	probable trpEG lea
83	1	9.1	11	2	S66196	alcohol dehydrogen
84	1	9.1	11	2	G42762	proteasome endopep
85	1	9.1	11	2	S68392	H+-transporting tw
86	1	9.1	11	2	B49164	chromogranin-B - r
87	1	9.1	11	2	S32575	ribosomal protein
88	1	9.1	11	2	PQ0682	photosystem I 17.5
89	1	9.1	11	2	S00616	parasporal crystal
90	1	9.1	11	2	C53652	rhlR protein - Pse
91	1	9.1	11	2	A57458	gene Gax protein -
92	1	9.1	11	2	A26930	ermG leader peptid
93	1	9.1	11	2	YHRT	morphogenetic neur
94	1	9.1	11	2	YHHU	morphogenetic neur
95	1	9.1	11	2	YHBO	morphogenetic neur
96	1	9.1	11	2	YHXAE	morphogenetic neur
97	1	9.1	11	2	YHJFHY	morphogenetic neur
98	1	9.1	11	2	A61365	phyllokinin - Rohd
99	1	9.1	11	2	S07207	Crinia-angiotensin
100	1	9.1	11	2	D61033	ranatachykinin D -

ALIGNMENTS

RESULT 1

S66606

quinoline 2-oxidoreductase alpha chain - Comamonas testosteroni (fragment)

C;Species: Comamonas testosteroni

C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S66606

R;Schach, S.; Tshisuaka, B.; Fetzner, S.; Lingens, F.

Eur. J. Biochem. 232, 536-544, 1995

A;Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from Comamonas testosteroni 63. The first two enzymes in quinoline and 3-methylquinoline degradation.

A;Reference number: S66606; MUID:96035889; PMID:7556204

A;Accession: S66606

A;Molecule type: protein

A;Residues: 1-11 <SCH>

A;Experimental source: strain 63

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.6e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 AKS 3

Db |||
 1 AKS 3

RESULT 2

H54346

pyruvate synthase (EC 1.2.7.1) alpha chain - Pyrococcus furiosus (fragment)

C;Species: Pyrococcus furiosus

C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-May-2000

C;Accession: H54346

R;Blamey, J.M.; Adams, M.W.

Biochemistry 33, 1000-1007, 1994

A;Title: Characterization of an ancestral type of pyruvate ferredoxin
oxidoreductase from the hyperthermophilic bacterium, Thermotoga maritima.

A;Reference number: A54346; MUID:94137707; PMID:8305426

A;Accession: H54346

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <BLA>

C;Keywords: coenzyme A; oxidoreductase

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KGN 7

|||

Db 4 KGN 6

RESULT 3

G61497

seed protein ws-23 - winged bean (fragment)

C;Species: Psophocarpus tetragonolobus (winged bean)

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C;Accession: G61497

R;Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A;Title: Microsequence analysis of winged bean seed proteins electroblotted from
two-dimensional gel.

A;Reference number: A61491; MUID:89351606; PMID:2765119

A;Accession: G61497

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <HIR>

C;Keywords: glycoprotein; seed

Query Match 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AKS 3

|||

Db 1 AKS 3

RESULT 4

ECLQ2M

tachykinin II - migratory locust

C;Species: Locusta migratoria (migratory locust)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 08-Dec-1995

C;Accession: S08266

R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; de Loof, A.
FEBS Lett. 261, 397-401, 1990

A;Title: Locustatachykinin I and II, two novel insect neuropeptides with
homology to peptides of the vertebrate tachykinin family.

A;Reference number: S08265; MUID:90184489; PMID:2311766

A;Accession: S08266

A;Molecule type: protein

A;Residues: 1-11 <SCH>

C;Superfamily: tachykinin

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 3e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9

||

Db 4 SS 5

RESULT 5

SPHO

substance P - horse

C;Species: Equus caballus (domestic horse)

C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996

C;Accession: A01558

R;Studer, R.O.; Trzeciak, A.; Lergier, W.
Helv. Chim. Acta 56, 860-866, 1973

A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.

A;Reference number: A01558

A;Accession: A01558

A;Molecule type: protein

A;Residues: 1-11 <STU>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 3e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11

||

Db 10 LM 11

RESULT 6

EOCC

eledoisin - curled octopus

C;Species: Eledone cirrosa, Ozaena cirrosa (curled octopus)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998

C;Accession: B01561; A01561
R;Anastasi, A.; Erspamer, V.
Arch. Biochem. Biophys. 101, 56-65, 1963
A;Title: The isolation and amino acid sequence of eledoisin, the active
endecapeptide of the posterior salivary glands of Eledone.
A;Reference number: A01561
A;Accession: B01561
A;Molecule type: protein
A;Residues: 1-11 <ANA>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland;
secretagogue; vasodilator; venom
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 7

A60654
substance P - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995
C;Accession: A60654
R;Murphy, R.
Neuropeptides 14, 105-110, 1989
A;Title: Primary amino acid sequence of guinea-pig substance P.
A;Reference number: A60654; MUID:90044685; PMID:2478925
A;Accession: A60654
A;Molecule type: protein
A;Residues: 1-11 <MUR>
C;Superfamily: substance P precursor
C;Keywords: amidated carboxyl end; neuropeptide; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 8

EOOC
eledoisin - musky octopus
C;Species: Eledone moschata, Ozaena moschata (musky octopus)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 20-Mar-1998
C;Accession: A01561
R;Anastasi, A.; Erspamer, V.

Arch. Biochem. Biophys. 101, 56-65, 1963

A;Title: The isolation and amino acid sequence of eledoisin, the active endecapeptide of the posterior salivary glands of Eledone.

A;Reference number: A01561

A;Accession: A01561

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone; pyroglutamic acid; salivary gland; secretagogue; vasodilator; venom

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 9

A33917

dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)

C;Species: Cricetulus griseus (Chinese hamster)

C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 07-Nov-1997

C;Accession: A33917

R;Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.T.; Evans, D.R.

Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989

A;Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain and interdomain linker in the CAD multifunctional polypeptide and properties of the isolated domain.

A;Reference number: A33917; MUID:89282776; PMID:2543974

A;Accession: A33917

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <SIM>

A;Cross-references: GB:M23652

C;Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; Bacillus dihydroorotase homology; biotin carboxylase homology; carbamoyl-phosphate synthase (ammonia) homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology; trpG homology

C;Keywords: hydrolase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KG 6
||
Db 7 KG 8

RESULT 10

JN0023

substance P - chicken

C;Species: Gallus gallus (chicken)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997

C;Accession: JN0023

R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A;Reference number: JN0023; MUID:88204263; PMID:2452461

A;Accession: JN0023

A;Molecule type: protein

A;Residues: 1-11 <CON>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11

||

Db 10 LM 11

RESULT 11

A40693

transgelin - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 31-Oct-1997

C;Accession: A40693

R;Shapland, C.; Hsuan, J.J.; Totty, N.F.; Lawson, D.

J. Cell Biol. 121, 1065-1073, 1993

A;Title: Purification and properties of transgelin: a transformation and shape change sensitive actin-gelling protein.

A;Reference number: A40693; MUID:93273790; PMID:8501116

A;Accession: A40693

A;Molecule type: protein

A;Residues: 1-11 <SHA>

A;Experimental source: aorta

C;Comment: This protein gels actin and is down regulated by transformation or loss of cell adherence in culture.

C;Superfamily: smooth muscle protein SM22; calponin repeat homology; smooth muscle protein SM22 homology

C;Keywords: actin binding; cytoskeleton

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KG 6

||

Db 1 KG 2

RESULT 12

A38841

rhodopsin homolog - squid (*Watasenia scintillans*) (fragment)
 N;Alternate names: visual pigment protein
 C;Species: *Watasenia scintillans* (sparkling enope)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Oct-1997
 C;Accession: A38841
 R;Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.
 Biochim. Biophys. Acta 957, 318-321, 1988
 A;Title: Amino acid sequence of the retinal binding site of squid visual pigment.
 A;Reference number: PT0063; MUID:89051045; PMID:3191148
 A;Accession: A38841
 A;Molecule type: protein
 A;Residues: 1-11 <SEI>
 C;Superfamily: vertebrate rhodopsin
 C;Keywords: chromoprotein; retinal
 F;3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 2 AK 3

RESULT 13

S09074

cytochrome P450-4b - rat (fragment)

N;Alternate names: cytochrome P450K-5

N;Contains: oxidoreductase (EC 1.-.-.-)

C;Species: *Rattus norvegicus* (Norway rat)

C;Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 05-Mar-1999

C;Accession: S09074

R;Imaoka, S.; Terano, Y.; Funae, Y.

Arch. Biochem. Biophys. 278, 168-178, 1990

A;Title: Changes in the amount of cytochrome P450s in rat hepatic microsomes with starvation.

A;Reference number: S09072; MUID:90210577; PMID:2321956

A;Accession: S09074

A;Molecule type: protein

A;Residues: 1-11 <IMA>

C;Superfamily: unassigned cytochrome P450; cytochrome P450 homology

C;Keywords: heme; microsome; monooxygenase; oxidoreductase; transmembrane protein

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
 ||
 Db 7 SL 8

RESULT 14

D60409

kassinin-like peptide K-III - frog (Pseudophryne guentheri)
 C;Species: Pseudophryne guentheri
 C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
 C;Accession: D60409
 R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;
 Melchiorri, P.; Erspamer, V.
 Peptides 11, 299-304, 1990
 A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog Pseudophryne guentheri.
 A;Reference number: A60409; MUID:90287814; PMID:2356157
 A;Accession: D60409
 A;Molecule type: protein
 A;Residues: 1-11 <SIM>
 C;Superfamily: unassigned animal peptides
 C;Keywords: amidated carboxyl end; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
 ||
 Db 10 LM 11

RESULT 15

F60409
 substance P-like peptide II - frog (Pseudophryne guentheri)
 C;Species: Pseudophryne guentheri
 C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000
 C;Accession: F60409
 R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;
 Melchiorri, P.; Erspamer, V.
 Peptides 11, 299-304, 1990
 A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of
 the Australian frog Pseudophryne guentheri.
 A;Reference number: A60409; MUID:90287814; PMID:2356157
 A;Accession: F60409
 A;Molecule type: protein
 A;Residues: 1-11 <SIM>
 C;Superfamily: unassigned animal peptides
 C;Keywords: amidated carboxyl end; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
 ||
 Db 10 LM 11

RESULT 16

E60409

substance P-like peptide I - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: E60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: E60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11

||

Db 10 LM 11

RESULT 17

B26744

megascoliakinin - garden dagger wasp

N;Alternate names: 6-Thr-bradykinin-Lys-Ala

C;Species: *Megascolia flavifrons* (garden dagger wasp)

C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000

C;Accession: B26744; A28609

R;Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.

Toxicon 25, 527-535, 1987

A;Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wasp *Megascolia flavifrons*.

A;Reference number: A94322; MUID:87293024; PMID:3617088

A;Accession: B26744

A;Molecule type: protein

A;Residues: 1-11 <YAS>

R;Nakajima, T.; Piek, T.; Yashuara, T.; Mantel, P.

Toxicon 26, 34, 1988

A;Title: Two kinins isolated from the venom of *Megascolia flavifrons*.

A;Reference number: A28609

A;Accession: A28609

A;Molecule type: protein

A;Residues: 1-11 <NAK>

C;Superfamily: unassigned animal peptides

C;Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 18.2%; Score 2; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 3e+04;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RK 5
||
Db 9 RK 10

RESULT 18

S23308

substance P - rainbow trout

C;Species: Oncorhynchus mykiss (rainbow trout)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23308

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23308

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 19

S23306

substance P - Atlantic cod

C;Species: Gadus morhua (Atlantic cod)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23306

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23306

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 20

B60409

kassinin-like peptide K-I - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000

C;Accession: B60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: B60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

A;Note: this peptide was also found in a deamidated form

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 21

C60409

kassinin-like peptide K-II - frog (*Pseudophryne guentheri*)

C;Species: *Pseudophryne guentheri*

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 18-Aug-2000

C;Accession: C60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.; Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Australian frog *Pseudophryne guentheri*.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: C60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
A;Note: this peptide was also found in a deamidated form
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 22

S07203

uperolein - frog (*Uperoleia marmorata*)

C;Species: *Uperoleia marmorata*

C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000

C;Accession: S07203

R;Anastasi, A.; Erspamer, V.; Endean, R.

Experientia 31, 394-395, 1975

A;Title: Structure of uperolein, a physalaemin-like endecapeptide occurring in the skin of *Uperoleia rugosa* and *Uperoleia marmorata*.

A;Reference number: S07203; MUID:75131227; PMID:1120493

A;Accession: S07203

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 23

S07201

physalaemin - frog (*Physalaemus fuscumaculatus*)

C;Species: *Physalaemus fuscumaculatus*

C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000

C;Accession: S07201

R;Erspamer, V.; Anastasi, A.; Bertaccini, G.; Cei, J.M.

Experientia 20, 489-490, 1964

A;Title: Structure and pharmacological actions of physalaemin, the main active polypeptide of the skin of *Physalaemus fuscumaculatus*.

A;Reference number: S07201; MUID:66076612; PMID:5857249

A;Accession: S07201
A;Molecule type: protein
A;Residues: 1-11 <ERS>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 24

A61033
ranatachykinin A - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
C;Accession: A61033; JE0426
R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.
Regul. Pept. 42(Suppl.1), S12, 1992
A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.
A;Reference number: A61033
A;Accession: A61033
A;Molecule type: protein
A;Residues: 1-11 <KAN>
R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
Biochem. Biophys. Res. Commun. 177, 588-595, 1991
A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.
A;Reference number: JE0426; MUID:91254337; PMID:2043143
A;Accession: JE0426
A;Molecule type: protein
A;Residues: 1-11 <KOZ>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; neuropeptide
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 25

B43669
hypothetical protein (rhdA 5' region) - Synechococcus sp. (fragment)
C;Species: Synechococcus sp.
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993

C;Accession: B43669
R;Laudenbach, D.E.; Ehrhardt, D.; Green, L.; Grossman, A.
J. Bacteriol. 173, 2751-2760, 1991
A;Title: Isolation and characterization of a sulfur-regulated gene encoding a periplasmically localized protein with sequence similarity to rhodanese.
A;Reference number: A43669; MUID:91210163; PMID:1708376
A;Accession: B43669
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-11 <LAU>
A;Cross-references: GB:M65244

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 6 AK 7

RESULT 26

PC2372

58K heat shock protein groEL [similarity] - Bacillus cereus (strain ts-4)
(fragment)

C;Species: Bacillus cereus

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C;Accession: PC2372

R;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.

Biosci. Biotechnol. Biochem. 59, 231-235, 1995

A;Title: Identification of DNA-binding proteins changed after induction of sporulation in Bacillus cereus.

A;Reference number: PC2369; MUID:95218265; PMID:7766022

A;Accession: PC2372

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <MAS>

C;Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 27

S19775

wound-induced protein - tomato (fragment)

C;Species: Lycopersicon esculentum (tomato)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997

C;Accession: S19775

R;Parsons, B.L.

submitted to the EMBL Data Library, May 1991

A;Reference number: S19773
A;Accession: S19775
A;Molecule type: mRNA
A;Residues: 1-11 <PAR>
A;Cross-references: EMBL:X59884; NID:g19323; PID:g19324

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 3 SS 4

RESULT 28

S71304

amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragment)

C;Species: Aspergillus niger

C;Date: 12-Feb-1998 #sequence_revision 01-May-1998 #text_change 07-May-1999

C;Accession: S71304

R;Frebort, I.; Tamaki, H.; Ishida, H.; Pec, P.; Luhova, L.; Tsuno, H.; Halata, M.; Asano, Y.; Kato, Y.; Matsushita, K.; Toyama, H.; Kumagai, H.; Adachi, O. Eur. J. Biochem. 237, 255-265, 1996

A;Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the mycelia of Aspergillus niger AKU 3302: purification, characterization, cDNA cloning and sequencing.

A;Reference number: S71303; MUID:96203933; PMID:8620882

A;Accession: S71304

A;Molecule type: protein

A;Residues: 1-11 <FRE>

C;Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquinone

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
||
Db 10 SL 11

RESULT 29

A34135

DNA-binding protein p - Crithidia fasciculata mitochondrion (fragment)

C;Species: mitochondrion Crithidia fasciculata

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999

C;Accession: A34135

R;Tittawella, I.

FEBS Lett. 260, 57-61, 1990

A;Title: Kinetoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fasciculata.

A;Reference number: A34135

A;Accession: A34135

A;Molecule type: protein

A;Residues: 1-11 <TIT>

C;Genetics:

A;Genome: mitochondrion
A;Genetic code: SGC6
C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RK 5
||
Db 8 RK 9

RESULT 30

A26120

6-phosphofructokinase (EC 2.7.1.11) - pig roundworm (fragment)

N;Alternate names: phosphofructokinase; phosphohexokinase

C;Species: Ascaris suum (pig roundworm)

C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 28-Apr-1993

C;Accession: A26120

R;Kulkarni, G.; Rao, G.S.J.; Srinivasan, N.G.; Hofer, H.W.; Yuan, P.M.; Harris, B.G.

J. Biol. Chem. 262, 32-34, 1987

A;Title: Ascaris suum phosphofructokinase. Phosphorylation by protein kinase and sequence of the phosphopeptide.

A;Reference number: A26120; MUID:87083467; PMID:3025208

A;Accession: A26120

A;Molecule type: protein

A;Residues: 1-11 <KUL>

C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 1 AK 2

RESULT 31

A35594

buccalin - California sea hare

C;Species: Aplysia californica (California sea hare)

C;Date: 14-Sep-1990 #sequence_revision 14-Sep-1990 #text_change 24-Jun-1993

C;Accession: A35594

R;Cropper, E.C.; Miller, M.W.; Tenenbaum, R.; Kolks, M.A.G.; Kupfermann, I.; Weiss, K.R.

Proc. Natl. Acad. Sci. U.S.A. 85, 6177-6181, 1988

A;Title: Structure and action of buccalin: a modulatory neuropeptide localized to an identified small cardioactive peptide-containing cholinergic motor neuron of Aplysia californica.

A;Reference number: A35594; MUID:88320404; PMID:3413086

A;Accession: A35594

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <CRO>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
||
Db 4 SL 5

RESULT 32

S69349

neuropeptide FFamide - great pond snail

C;Species: *Lymnaea stagnalis* (great pond snail)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-1999

C;Accession: S69349

R;Li, K.W.; El Filali, Z.; van Golen, F.A.; Geraerts, W.P.M.

Eur. J. Biochem. 229, 70-72, 1995

A;Title: Identification of a novel amide peptide, GLTPNMNSLFF-NH(2), involved in the control of vas deferens motility in *Lymnaea stagnalis*.

A;Reference number: S69349; MUID:95262689; PMID:7744051

A;Accession: S69349

A;Molecule type: protein

A;Residues: 1-11 <LIK>

A;Experimental source: penis complex

C;Function:

A;Description: enhances the contraction frequency and contraction amplitude of the vas deferens

A;Note: control of male reproductive behavior

C;Keywords: amidated carboxyl end; neuropeptide

F;11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NS 8
||
Db 7 NS 8

RESULT 33

S05002

corazonin - American cockroach

C;Species: *Periplaneta americana* (American cockroach)

C;Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Apr-1998

C;Accession: S05002

R;Veenstra, J.A.

FEBS Lett. 250, 231-234, 1989

A;Title: Isolation and structure of corazonin, a cardioactive peptide from the american cockroach.

A;Reference number: S05002; MUID:89325572; PMID:2753132

A;Accession: S05002

A;Molecule type: protein

A;Residues: 1-11 <VEE>

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 6 SR 7

RESULT 34

S33300

probable substance P - smaller spotted catshark

C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999

C;Accession: S33300

R;Waugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.

Eur. J. Biochem. 214, 469-474, 1993

A;Title: Primary structures and biological activities of substance-P-related peptides from the brain of the dogfish, Scyliorhinus canicula.

A;Reference number: S33300; MUID:93292508; PMID:7685693

A;Accession: S33300

A;Molecule type: protein

A;Residues: 1-11 <WAU>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of preprotachykinin A

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 35

S43626

cytochrome-c oxidase (EC 1.9.3.1) chain Vb-H - trout (fragment)

C;Species: Salmo sp. (trout)

C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 02-Jul-1998

C;Accession: S43626

R;Freund, R.; Kadenbach, B.

Eur. J. Biochem. 221, 1111-1116, 1994

A;Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase isolated from rainbow trout.

A;Reference number: S43624; MUID:94237150; PMID:8181469

A;Accession: S43626

A;Status: preliminary

A;Molecule type: protein
A;Residues: 1-11 <FRE>
C;Keywords: electron transfer; membrane-associated complex; oxidoreductase;
respiratory chain; transmembrane protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KG 6
||
Db 4 KG 5

RESULT 36

D42965

talín - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996

C;Accession: D42965

R;Hagmann, J.; Grob, M.; Burger, M.M.

J. Biol. Chem. 267, 14424-14428, 1992

A;Title: The cytoskeletal protein talín is O-glycosylated.

A;Reference number: A42965; MUID:92332560; PMID:1629228

A;Accession: D42965

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <HAG>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 4 SS 5

RESULT 37

I65231

CCK-B gastrin receptor isoform - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C;Accession: I65231

R;Miyake, A.

Biochem. Biophys. Res. Commun. 208, 230-237, 1995

A;Title: A truncated isoform of human CCK-B/gastrin receptor generated by
alternative usage of a novel exon.

A;Reference number: I52307; MUID:95194412; PMID:7887934

A;Accession: I65231

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-11 <RES>

A;Cross-references: GB:S76072; NID:g913752; PIDN:AAB33740.1; PID:g913753

C;Genetics:

A;Gene: CCK-B

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GN 7
||
Db 5 GN 6

RESULT 38

E57789

gallbladder stone matrix protein, 25K - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996

C;Accession: E57789

R;Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, February 1996

A;Description: The proteins of gallbladder stones.

A;Reference number: A57789

A;Accession: E57789

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <BIN>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RK 5
||
Db 2 RK 3

RESULT 39

I52980

glucocerebrosidase - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C;Accession: I52980; I65971

R;Reiner, O.; Wigderson, M.; Horowitz, M.

DNA 7, 107-116, 1988

A;Title: Structural analysis of the human glucocerebrosidase genes.

A;Reference number: I52980; MUID:88195776; PMID:3359914

A;Accession: I52980

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <RES>

A;Cross-references: GB:M18916; NID:g183023; PIDN:AAA35878.1; PID:g183024

A;Accession: I65971

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <RE2>

A;Cross-references: GB:M18917; NID:g183025; PIDN:AAA35879.1; PID:g183026

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 4 SS 5

RESULT 40

PT0273

Ig heavy chain CRD3 region (clone 3-109A) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0273

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain
diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0273

A;Molecule type: DNA

A;Residues: 1-11 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 2 SR 3

RESULT 41

PT0302

Ig heavy chain CRD3 region (clone 5-112) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0302

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain
diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0302

A;Molecule type: DNA

A;Residues: 1-11 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 7 SS 8

RESULT 42

S13279

Ile-Ser-bradykinin - human (fragment)

N;Alternate names: T-kinin

C;Species: Homo sapiens (man)

C;Date: 02-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 24-Jul-1998

C;Accession: S13279

R;Wunderer, G.; Walter, I.; Eschenbacher, B.; Lang, M.; Kellermann, J.; Kindermann, G.

Biol. Chem. Hoppe-Seyler 371, 977-981, 1990

A;Title: Ile-Ser-bradykinin is an aberrant permeability factor in various human malignant effusions.

A;Reference number: S13279; MUID:91166748; PMID:2076202

A;Accession: S13279

A;Molecule type: protein

A;Residues: 1-11 <WUN>

C;Keywords: bradykinin

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 2 SR 3

RESULT 43

I54193

Rhesus blood group CcEe protein - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000

C;Accession: I54193

R;Cherif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.; Colin, Y.

Genomics 19, 68-74, 1994

A;Title: Organization of the gene (RHCE) encoding the human blood group RhCcEe antigens and characterization of the promoter region.

A;Reference number: I54193; MUID:94245182; PMID:8188244

A;Accession: I54193

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-11 <RES>

A;Cross-references: GB:S70456; NID:g546795; PIDN:AAD14061.1; PID:g4261761

C;Genetics:

A;Gene: GDB:RHCE

A;Cross-references: GDB:229957; OMIM:111700

A;Map position: 1p36.2-1p34

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 2 SS 3

RESULT 44

S68649

spermadhesin AQN-3 - pig (fragments)

C;Species: *Sus scrofa domestica* (domestic pig)

C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 17-Mar-1999

C;Accession: S68649

R;Calvete, J.J.; Dostalova, Z.; Sanz, L.; Adermann, K.; Thole, H.H.; Toepfer-Petersen, E.

FEBS Lett. 379, 207-211, 1996

A;Title: Mapping the heparin-binding domain of boar spermadhesins.

A;Reference number: S68648; MUID:96184566; PMID:8603690

A;Accession: S68649

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-6;7-11 <CAL>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 10 SS 11

RESULT 45

S68637

acetylcholinesterase (EC 3.1.1.7) P chain - bovine (fragment)

C;Species: *Bos primigenius taurus* (cattle)

C;Date: 04-Dec-1997 #sequence_revision 04-Dec-1997 #text_change 30-Jan-1998

C;Accession: S68637

R;Boschetti, N.; Brodbeck, U.

FEBS Lett. 380, 133-136, 1996

A;Title: The membrane anchor of mammalian brain acetylcholinesterase consists of a single glycosylated protein of 22 kDa.

A;Reference number: S68637; MUID:96181683; PMID:8603722

A;Accession: S68637

A;Molecule type: protein

A;Residues: 1-11 <BOS>

A;Experimental source: brain

C;Keywords: carboxylic ester hydrolase; glycoprotein; membrane protein

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KS 3
||
Db 4 KS 5

RESULT 46

A33571

follistatin - bovine (fragment)

C;Species: *Bos primigenius taurus* (cattle)

C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 30-Sep-1993
C;Accession: A33571
R;Gospodarowicz, D.; Lau, K.
Biochem. Biophys. Res. Commun. 165, 292-298, 1989
A;Title: Pituitary follicular cells secrete both vascular endothelial growth factor and follistatin.
A;Reference number: A33571; MUID:90073725; PMID:2590228
A;Accession: A33571
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <GOS>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 8 AK 9

RESULT 47

S23926

major glycoprotein PAS-6 - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999

C;Accession: S23926

R;Kim, D.H.; Kanno, C.; Mizokami, Y.

Biochim. Biophys. Acta 1122, 203-211, 1992

A;Title: Purification and characterization of major glycoproteins, PAS-6 and PAS-7, from bovine milk fat globule membrane.

A;Reference number: S23926; MUID:92353107; PMID:1643094

A;Accession: S23926

A;Molecule type: protein

A;Residues: 1-11 <KIM>

C;Keywords: glycoprotein; milk; blocked amino end

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GN 7
||
Db 3 GN 4

RESULT 48

A14454

6-phosphofructokinase (EC 2.7.1.11) - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 28-Apr-1993

C;Accession: A14454

R;Fordyce, A.M.; Midwinter, G.G.; Moore, C.H.

Biochem. Soc. Trans. 7, 721-723, 1979

A;Title: The N-terminal amino acid sequence of sheep heart phosphofructokinase.

A;Reference number: A14454; MUID:80004524; PMID:157899

A;Accession: A14454

A;Molecule type: protein
A;Residues: 1-11 <FOR>
C;Keywords: glycolysis; phosphotransferase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 8 AK 9

RESULT 49

A29806

acidic proline-rich protein HP43b - golden hamster (fragment)

C;Species: Mesocricetus auratus (golden hamster)

C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993

C;Accession: A29806

R;Mehansho, H.; Ann, D.K.; Butler, L.G.; Rogler, J.; Carlson, D.M.

J. Biol. Chem. 262, 12344-12350, 1987

A;Title: Induction of proline-rich proteins in hamster salivary glands by isoproterenol treatment and an unusual growth inhibition by tannins.

A;Reference number: A92611; MUID:87308247; PMID:3040740

A;Accession: A29806

A;Molecule type: protein

A;Residues: 1-11 <MEH>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
||
Db 10 SL 11

RESULT 50

PH1375

T antigen variant K-2 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000

C;Accession: PH1375

R;Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.

J. Exp. Med. 176, 449-457, 1992

A;Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for transformed cells with point mutations within sequences encoding CTL recognition epitopes.

A;Reference number: PH1373; MUID:92364547; PMID:1380062

A;Accession: PH1375

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <LIL>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KG 6
||
Db 2 KG 3

RESULT 51

PH1376

T antigen variant K-3 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000

C;Accession: PH1376

R;Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.

J. Exp. Med. 176, 449-457, 1992

A;Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for transformed cells with point mutations within sequences encoding CTL recognition epitopes.

A;Reference number: PH1373; MUID:92364547; PMID:1380062

A;Accession: PH1376

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <LIL>

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KG 6
||
Db 2 KG 3

RESULT 52

PT0217

T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0217

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0217

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 3 SR 4

RESULT 53

PT0218

T-cell receptor beta chain V-J region (7-10-D.3) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C;Accession: PT0218

R;Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A;Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted in non-obese diabetic mice.

A;Reference number: PT0209; MUID:91217621; PMID:1902501

A;Accession: PT0218

A;Molecule type: mRNA

A;Residues: 1-11 <NAK>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GN 7
 ||
Db 7 GN 8

RESULT 54

D41946

T-cell receptor gamma chain (1a.4) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C;Accession: D41946

R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma genes in intestinal intraepithelial lymphocytes from murine athymic chimeras.

A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: D41946

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-11 <WHE>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
 ||
Db 8 SS 9

RESULT 55

B41946

T-cell receptor gamma chain (1t.57) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: B41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma genes in intestinal intraepithelial lymphocytes from murine athymic chimeras.
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: B41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-11 <WHE>
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 8 SS 9

RESULT 56

C38887

T-cell receptor gamma chain (5a.3) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C;Accession: C38887

R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma genes in intestinal intraepithelial lymphocytes from murine athymic chimeras.

A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: C38887

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-11 <WHE>

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 8 SS 9

RESULT 57

I41946

T-cell receptor gamma chain (5t.1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C;Accession: I41946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma genes in intestinal intraepithelial lymphocytes from murine athymic chimeras.
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: I41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-11 <WHE>
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 8 SS 9

RESULT 58

PD0441

translation elongation factor TU-like protein P43, mitochondrial - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Aug-1998

C;Accession: PD0441

R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A. submitted to JIPID, August 1998

A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Accession: PD0441

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: striatum

C;Keywords: mitochondrion

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 4 AK 5

RESULT 59

I60434

68kDa neurofilament - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999

C;Accession: I60434

R;Reeben, M.; Neuman, T.; Palgi, J.; Palm, K.; Paalme, V.; Saarma, M. J. Neurosci. Res. 40, 177-188, 1995

A;Title: Characterization of the rat light neurofilament (NF-L) gene promoter and identification of NGF and cAMP responsive regions.
A;Reference number: I60434; MUID:95264348; PMID:7745611
A;Accession: I60434
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-11 <RES>
A;Cross-references: EMBL:X53981; NID:g452676; PIDN:CAA37931.1; PID:g452677
C;Genetics:
A;Gene: NF68

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 2 SS 3

RESULT 60
S65377

cytochrome-c oxidase (EC 1.9.3.1) chain VIa-H, cardiac - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: S65377
R;Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A;Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the adult liver isoform.
A;Reference number: S65372; MUID:95324529; PMID:7601105
A;Accession: S65377
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <SCH>
C;Keywords: cardiac muscle; heart; oxidoreductase

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 3 AK 4

RESULT 61
PH0939

T-cell receptor beta chain V-D-J region (clone 10) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0939
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0939
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 3 SS 4

RESULT 62

PH0940

T-cell receptor beta chain V-D-J region (clone 11) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0940
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0940
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 3 SS 4

RESULT 63

PH0941

T-cell receptor beta chain V-D-J region (clone 12) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0941
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0941
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 3 SS 4

RESULT 64

PH0929

T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0929

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0929

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 3 SR 4

RESULT 65

PH0891

T-cell receptor beta chain V-D-J region (clone 6-1) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0891

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0891

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized T-cell

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 3 SS 4

RESULT 66

PH0938

T-cell receptor beta chain V-D-J region (clone 9) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0938

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0938

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: complete Freund's adjuvant-immunized lymph node

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 3 SS 4

RESULT 67

PH0947

T-cell receptor beta chain V-D-J region (clone A2) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0947

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0947

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein fragment-reactive T-cell, recovered from experimentally induced allergic encephalomyelitis

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 3 SR 4

RESULT 68

PH0903

T-cell receptor beta chain V-D-J region (hybridoma S1C2A6) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0903

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0903

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized T-cell

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 3 SS 4

RESULT 69

PH0904

T-cell receptor beta chain V-D-J region (hybridoma S22C2) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0904

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandembark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0904

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized T-cell

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 3 SS 4

RESULT 70

PH0924

T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0924
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0924
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 3 SS 4

RESULT 71

PH0919

T-cell receptor beta chain V-D-J region (isolate 5) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0919
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental
allergic encephalomyelitis: conserved complementarity determining region 3.
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0919
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
A;Note: the authors translated the codon CAG for residue 11 as Glu
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 3 SR 4

RESULT 72

PH0914

T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0914
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0914

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: myelin basic protein-immunized lymph node

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 3 SS 4

RESULT 73

PH0922

T-cell receptor beta chain V-D-J region (isolate 8) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0922

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0922

A;Molecule type: mRNA

A;Residues: 1-11 <GOL>

A;Experimental source: concanavalin A-activated lymphoblast

C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 3 SS 4

RESULT 74

PH0906

T-cell receptor beta chain V-D-J region (isolates 2, 8, 9) - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C;Accession: PH0906

R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis: conserved complementarity determining region 3.

A;Reference number: PH0891; MUID:92078857; PMID:1836012

A;Accession: PH0906

A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: myelin basic protein-immunized lymph node
C;Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 3 SS 4

RESULT 75

A34243

H-hyosophorin - Japanese flounder (fragment)

C;Species: Paralichthys olivaceus (Japanese flounder)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 12-Feb-1999

C;Accession: A34243

R;Seko, A.; Kitajima, K.; Iwasaki, M.; Inoue, S.; Inoue, Y.

J. Biol. Chem. 264, 15922-15929, 1989

A;Title: Structural studies of fertilization-associated carbohydrate-rich glycoproteins (Hyosophorin) isolated from the fertilized and unfertilized eggs of flounder, Paralichthys olivaceus. Presence of a novel penta-antennary N-linked glycan chain in the tandem repeating glycopeptide unit of hyosophorin.

A;Reference number: A34243; MUID:89380184; PMID:2777771

A;Accession: A34243

A;Molecule type: protein

A;Residues: 1-11 <SEK>

A;Note: 3-Ala, 4-Ala, 5-Pro or Gln, and 6-Val were also found

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GN 7
||
Db 6 GN 7

Search completed: April 8, 2004, 15:49:28

Job time : 8.61538 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:47:33 ; Search time 30.3077 Seconds
(without alignments)
95.432 Million cell updates/sec

Title: US-09-787-443A-21
Perfect score: 11
Sequence: 1 AKSRKGNSSLM 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9223

Minimum DB seq length: 11
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score Match Length DB ID	Description

1	4	36.4	11	10	US-09-876-904A-83	Sequence 83, Appl
2	4	36.4	11	14	US-10-211-088-246	Sequence 246, App
3	3	27.3	11	8	US-08-779-457-43	Sequence 43, Appl
4	3	27.3	11	9	US-09-780-070-25	Sequence 25, Appl
5	3	27.3	11	9	US-09-780-070-26	Sequence 26, Appl
6	3	27.3	11	9	US-09-823-649A-18	Sequence 18, Appl
7	3	27.3	11	9	US-09-056-160B-17	Sequence 17, Appl
8	3	27.3	11	9	US-09-896-251-11	Sequence 11, Appl
9	3	27.3	11	9	US-09-896-251-18	Sequence 18, Appl
10	3	27.3	11	9	US-09-896-245-11	Sequence 11, Appl
11	3	27.3	11	9	US-09-896-245-18	Sequence 18, Appl
12	3	27.3	11	9	US-09-935-682-28	Sequence 28, Appl
13	3	27.3	11	9	US-09-873-637-13	Sequence 13, Appl
14	3	27.3	11	9	US-09-825-584-1	Sequence 1, Appli
15	3	27.3	11	9	US-09-192-854-170	Sequence 170, App
16	3	27.3	11	9	US-09-811-384-8	Sequence 8, Appli
17	3	27.3	11	9	US-09-832-723-35	Sequence 35, Appl
18	3	27.3	11	9	US-09-226-248B-27	Sequence 27, Appl
19	3	27.3	11	9	US-09-966-871-31	Sequence 31, Appl
20	3	27.3	11	9	US-09-848-664-6	Sequence 6, Appli
21	3	27.3	11	9	US-09-071-838-286	Sequence 286, App
22	3	27.3	11	9	US-09-968-561A-298	Sequence 298, App
23	3	27.3	11	9	US-09-969-244-11	Sequence 11, Appl
24	3	27.3	11	9	US-09-969-244-18	Sequence 18, Appl
25	3	27.3	11	9	US-09-757-774-13	Sequence 13, Appl
26	3	27.3	11	10	US-09-999-724-76	Sequence 76, Appl
27	3	27.3	11	10	US-09-876-904A-369	Sequence 369, App
28	3	27.3	11	10	US-09-876-904A-509	Sequence 509, App
29	3	27.3	11	10	US-09-774-381-59	Sequence 59, Appl
30	3	27.3	11	10	US-09-852-910-259	Sequence 259, App
31	3	27.3	11	10	US-09-802-083-14	Sequence 14, Appl
32	3	27.3	11	10	US-09-776-191-59	Sequence 59, Appl
33	3	27.3	11	10	US-09-968-744A-298	Sequence 298, App
34	3	27.3	11	11	US-09-795-798-16	Sequence 16, Appl
35	3	27.3	11	11	US-09-969-322-11	Sequence 11, Appl
36	3	27.3	11	11	US-09-969-322-18	Sequence 18, Appl
37	3	27.3	11	11	US-09-833-245-301	Sequence 301, App
38	3	27.3	11	12	US-09-968-561A-298	Sequence 298, App
39	3	27.3	11	12	US-10-289-456-91	Sequence 91, Appl
40	3	27.3	11	12	US-10-417-895A-63	Sequence 63, Appl
41	3	27.3	11	12	US-10-417-895A-66	Sequence 66, Appl
42	3	27.3	11	12	US-10-356-824-3	Sequence 3, Appli
43	3	27.3	11	12	US-10-430-685-35	Sequence 35, Appl
44	3	27.3	11	12	US-10-430-685-37	Sequence 37, Appl
45	3	27.3	11	12	US-10-430-685-39	Sequence 39, Appl
46	3	27.3	11	12	US-10-600-152-3	Sequence 3, Appli
47	3	27.3	11	12	US-10-609-217-980	Sequence 980, App
48	3	27.3	11	12	US-10-398-104-179	Sequence 179, App
49	3	27.3	11	12	US-10-458-860-31	Sequence 31, Appl
50	3	27.3	11	12	US-10-149-135-15	Sequence 15, Appl
51	3	27.3	11	12	US-10-149-135-59	Sequence 59, Appl
52	3	27.3	11	12	US-10-149-135-83	Sequence 83, Appl
53	3	27.3	11	12	US-10-149-135-217	Sequence 217, App
54	3	27.3	11	12	US-10-149-135-278	Sequence 278, App
55	3	27.3	11	12	US-10-149-135-406	Sequence 406, App
56	3	27.3	11	12	US-10-149-135-409	Sequence 409, App

57	3	27.3	11	12	US-10-149-135-414	Sequence 414, App
58	3	27.3	11	12	US-10-149-135-469	Sequence 469, App
59	3	27.3	11	12	US-10-149-135-506	Sequence 506, App
60	3	27.3	11	12	US-10-149-135-699	Sequence 699, App
61	3	27.3	11	12	US-10-149-135-738	Sequence 738, App
62	3	27.3	11	12	US-10-149-135-843	Sequence 843, App
63	3	27.3	11	12	US-10-149-135-878	Sequence 878, App
64	3	27.3	11	12	US-10-149-135-903	Sequence 903, App
65	3	27.3	11	12	US-10-149-135-905	Sequence 905, App
66	3	27.3	11	12	US-10-149-135-912	Sequence 912, App
67	3	27.3	11	12	US-10-149-135-948	Sequence 948, App
68	3	27.3	11	12	US-10-149-135-961	Sequence 961, App
69	3	27.3	11	12	US-10-149-135-991	Sequence 991, App
70	3	27.3	11	12	US-10-149-135-999	Sequence 999, App
71	3	27.3	11	12	US-10-149-135-1018	Sequence 1018, Ap
72	3	27.3	11	12	US-10-149-135-1020	Sequence 1020, Ap
73	3	27.3	11	12	US-10-149-135-1041	Sequence 1041, Ap
74	3	27.3	11	12	US-10-149-135-1049	Sequence 1049, Ap
75	3	27.3	11	12	US-10-149-135-1057	Sequence 1057, Ap
76	3	27.3	11	12	US-10-149-135-1059	Sequence 1059, Ap
77	3	27.3	11	12	US-10-149-135-1253	Sequence 1253, Ap
78	3	27.3	11	12	US-10-149-135-1303	Sequence 1303, Ap
79	3	27.3	11	12	US-10-149-135-1322	Sequence 1322, Ap
80	3	27.3	11	12	US-10-149-135-1356	Sequence 1356, Ap
81	3	27.3	11	12	US-10-149-135-1399	Sequence 1399, Ap
82	3	27.3	11	12	US-10-149-135-1498	Sequence 1498, Ap
83	3	27.3	11	12	US-10-149-135-1515	Sequence 1515, Ap
84	3	27.3	11	12	US-10-149-135-1525	Sequence 1525, Ap
85	3	27.3	11	12	US-10-149-135-1539	Sequence 1539, Ap
86	3	27.3	11	12	US-10-149-135-1596	Sequence 1596, Ap
87	3	27.3	11	12	US-10-149-135-1669	Sequence 1669, Ap
88	3	27.3	11	12	US-10-149-135-1689	Sequence 1689, Ap
89	3	27.3	11	12	US-10-149-135-1768	Sequence 1768, Ap
90	3	27.3	11	12	US-10-149-135-1785	Sequence 1785, Ap
91	3	27.3	11	12	US-10-149-135-1794	Sequence 1794, Ap
92	3	27.3	11	12	US-10-149-135-1895	Sequence 1895, Ap
93	3	27.3	11	12	US-10-149-135-2256	Sequence 2256, Ap
94	3	27.3	11	12	US-10-398-616-4	Sequence 4, Appli
95	3	27.3	11	12	US-10-398-616-10	Sequence 10, Appl
96	3	27.3	11	12	US-10-632-388-980	Sequence 980, App
97	3	27.3	11	12	US-10-404-286-8	Sequence 8, Appli
98	3	27.3	11	12	US-10-433-596-11	Sequence 11, Appl
99	3	27.3	11	12	US-10-433-596-18	Sequence 18, Appl
100	3	27.3	11	12	US-10-651-723-980	Sequence 980, App

ALIGNMENTS

RESULT 1

US-09-876-904A-83

; Sequence 83, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
 ; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
 ; FILE REFERENCE: TB-2002.00
 ; CURRENT APPLICATION NUMBER: US/09/876,904A
 ; CURRENT FILING DATE: 2001-06-08
 ; PRIOR APPLICATION NUMBER: US 60/210,925
 ; PRIOR FILING DATE: 2000-06-09
 ; NUMBER OF SEQ ID NOS: 629
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 83
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic T-DNA-linked VirD2
 ; OTHER INFORMATION: endonuclease of the Agrobacterium tumefaciens tumor-inducing
 ; OTHER INFORMATION: plasmid
 US-09-876-904A-83

Query Match 36.4%; Score 4; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRKG 6
 ||||
 Db 4 SRKG 7

RESULT 2

US-10-211-088-246
 ; Sequence 246, Application US/10211088
 ; Publication No. US20030104479A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bright, Gary R.
 ; APPLICANT: Premkumar, D. David
 ; APPLICANT: Chen, Yih-Tai
 ; TITLE OF INVENTION: No. US20030104479A1el Fusion Proteins And Assays For Molecular Binding
 ; FILE REFERENCE: 01-1022-US
 ; CURRENT APPLICATION NUMBER: US/10/211,088
 ; CURRENT FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: 60/309,395
 ; PRIOR FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: 60/341,589
 ; PRIOR FILING DATE: 2001-12-13
 ; NUMBER OF SEQ ID NOS: 366
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 246
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Nuclear localization signal
 US-10-211-088-246

Query Match 36.4%; Score 4; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRKG 6
||||
Db 4 SRKG 7

RESULT 3

US-08-779-457-43

; Sequence 43, Application US/08779457

; Publication No. US20020193571A1

; GENERAL INFORMATION:

; APPLICANT: Carter, Paul J.

; APPLICANT: Chiang, Nancy Y.

; APPLICANT: Kyung, Jin Kim

; APPLICANT: Matthews, William

; APPLICANT: Rodrigues, Maria L.

; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/779,457

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/667197

; FILING DATE: 06/20/96

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/585005

; FILING DATE: 01/08/96

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378

; REFERENCE/DOCKET NUMBER: P0986P2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

US-08-779-457-43

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 3 NSS 5

RESULT 4

US-09-780-070-25

; Sequence 25, Application US/09780070

; Patent No. US20020009752A1

; GENERAL INFORMATION:

; APPLICANT: Burke, James

; APPLICANT: Strittmater, Warren

; APPLICANT: Nagai, Yoshitaka

; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE
REPEAT DOMAINS

; TITLE OF INVENTION: AND METHODS OF USE THEREOF

; FILE REFERENCE: 5405.242

; CURRENT APPLICATION NUMBER: US/09/780,070

; CURRENT FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/189,781

; PRIOR FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 25

; LENGTH: 11

; TYPE: PRT

; ORGANISM: synthetic construct

US-09-780-070-25

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KGN 7
|||
Db 6 KGN 8

RESULT 5

US-09-780-070-26

; Sequence 26, Application US/09780070

; Patent No. US20020009752A1

; GENERAL INFORMATION:

; APPLICANT: Burke, James

; APPLICANT: Strittmater, Warren

; APPLICANT: Nagai, Yoshitaka

; TITLE OF INVENTION: COMPOUNDS THAT SELECTIVELY BIND TO EXPANDED POLYGLUTAMINE
REPEAT DOMAINS

; TITLE OF INVENTION: AND METHODS OF USE THEREOF

; FILE REFERENCE: 5405.242

; CURRENT APPLICATION NUMBER: US/09/780,070

; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/189,781
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-780-070-26

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SLM 11
 | | |
Db 2 SLM 4

RESULT 6

US-09-823-649A-18

; Sequence 18, Application US/09823649A
; Patent No. US20020012970A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Edward
; APPLICANT: Elfstrom, Carita
; APPLICANT: Gelfand, David
; APPLICANT: Higuchi, Russell
; APPLICANT: Myers, Thomas
; APPLICANT: Schoenbrunner, Nancy
; APPLICANT: Wang, Alice
; TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA
POLYMERASES
; FILE REFERENCE: RPA1006
; CURRENT APPLICATION NUMBER: US/09/823,649A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/198,336
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Bacillus caldotenax
US-09-823-649A-18

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
 | | |
Db 8 SRK 10

RESULT 7

US-09-056-160B-17
; Sequence 17, Application US/09056160B
; Patent No. US20020032315A1
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; APPLICANT: Wells, James A.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Chen, Yvonne M.
; TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
; NUMBER OF SEQUENCES: 131
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,160B
; FILING DATE: 06-Apr-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/054,856
; FILING DATE: 06-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1093R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-056-160B-17

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 3 NSS 5

RESULT 8
US-09-896-251-11
; Sequence 11, Application US/09896251
; Patent No. US20020041880A1

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; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: DeFeo-Jones, Deborah
; APPLICANT: Heimbroom, David C.
; APPLICANT: Jones, Raymond E.
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 20662
; CURRENT APPLICATION NUMBER: US/09/896,251
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,934
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(1)
; OTHER INFORMATION: acetylated N-terminus amino acid
US-09-896-251-11
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Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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QY      8 SSL 10
      |||
Db      9 SSL 11
```

RESULT 9

US-09-896-251-18

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; Sequence 18, Application US/09896251
; Patent No. US20020041880A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: DeFeo-Jones, Deborah
; APPLICANT: Heimbroom, David C.
; APPLICANT: Jones, Raymond E.
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 20662
; CURRENT APPLICATION NUMBER: US/09/896,251
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,934
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
; NAME/KEY: AMIDATION
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; LOCATION: (11)...(11)
; OTHER INFORMATION: leucinamide
US-09-896-251-18

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 9 SSL 11

RESULT 10

US-09-896-245-11
; Sequence 11, Application US/09896245
; Patent No. US20020042375A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Heimbrosk, David C.
; APPLICANT: Yao, Siu-Long
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 20664Y
; CURRENT APPLICATION NUMBER: US/09/896,245
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/216,217
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(1)
; OTHER INFORMATION: acetylated N-terminus amino acid
US-09-896-245-11

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 9 SSL 11

RESULT 11

US-09-896-245-18
; Sequence 18, Application US/09896245
; Patent No. US20020042375A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Heimbrosk, David C.
; APPLICANT: Yao, Siu-Long

```
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 20664Y
; CURRENT APPLICATION NUMBER: US/09/896,245
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/216,217
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
; NAME/KEY: AMIDATION
; LOCATION: (11)...(11)
; OTHER INFORMATION: leucinamide
US-09-896-245-18
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```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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```
Qy      8 SSL 10
        |||
Db      9 SSL 11
```

RESULT 12

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US-09-935-682-28
; Sequence 28, Application US/09935682
; Patent No. US20020059032A1
; GENERAL INFORMATION:
; APPLICANT: Societe de Conseils de Recherches et D'Applications Scientifiques
; APPLICANT: Ferrer, Camara Y.
; TITLE OF INVENTION: Rational Selection of Putative Peptides from Identified
Nucleotide or
; TITLE OF INVENTION: Peptide Sequences
; FILE REFERENCE: 58767.000005
; CURRENT APPLICATION NUMBER: US/09/935,682
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/257,525
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: PCT/FR00/00460
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-682-28
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Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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Qy 9 SLM 11
|||
Db 2 SLM 4

RESULT 13

US-09-873-637-13

; Sequence 13, Application US/09873637
; Patent No. US20020061543A1
; GENERAL INFORMATION:
; APPLICANT: Ross, Jeffrey
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
; FILE REFERENCE: 960296.95131
; CURRENT APPLICATION NUMBER: US/09/873,637
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-873-637-13

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 3 SSL 5

RESULT 14

US-09-825-584-1

; Sequence 1, Application US/09825584
; Patent No. US20020064805A1
; GENERAL INFORMATION:
; APPLICANT: Akita, Robert
; Sliwkowski, Mark
; TITLE OF INVENTION: ErbB3 Antibodies
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/825,584
; FILING DATE: 04-Apr-2001

```

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/827,009
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1003R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-825-584-1

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      7 NSS 9
      |||
Db      3 NSS 5

```

RESULT 15

```

US-09-192-854-170
; Sequence 170, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 170
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-170

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      8 SSL 10
      |||
Db      8 SSL 10

```

RESULT 16
 US-09-811-384-8
 ; Sequence 8, Application US/09811384
 ; Patent No. US20020081294A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bednar, Martin M.
 ; Thomas, G. Roger
 ; Gross, Cordell E.
 ; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/811,384
 ; FILING DATE: 20-Dec-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/251652
 ; FILING DATE: 17-FEB-2000
 ; APPLICATION NUMBER: 08/788800
 ; FILING DATE: 22-JAN-1997
 ; APPLICATION NUMBER: 60/093038
 ; FILING DATE: 23-JAN-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Love, Richard B.
 ; REGISTRATION NUMBER: 34,659
 ; REFERENCE/DOCKET NUMBER: P1729C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-5530
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-811-384-8

Query Match 27.3%; Score 3; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
 |||
 Db 3 NSS 5

RESULT 17

US-09-832-723-35

; Sequence 35, Application US/09832723
 ; Patent No. US20020098524A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Estell, David A.
 ; APPLICANT: Chen, Yiyou
 ; APPLICANT: Murray, Christopher J.
 ; APPLICANT: Tijerina, Pilar
 ; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
 ; FILE REFERENCE: GC617-2
 ; CURRENT APPLICATION NUMBER: US/09/832,723
 ; CURRENT FILING DATE: 2001-04-11
 ; PRIOR APPLICATION NUMBER: US 60/197,259
 ; PRIOR FILING DATE: 2000-04-14
 ; NUMBER OF SEQ ID NOS: 117
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 35
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptides screened from a phage display random
 ; OTHER INFORMATION: peptide library
 US-09-832-723-35

Query Match 27.3%; Score 3; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SLM 11
 |||
 Db 5 SLM 7

RESULT 18

US-09-226-248B-27

; Sequence 27, Application US/09226248B
 ; Patent No. US20020106690A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEBERER, Ekkehard
 ; APPLICANT: LEEUW, Thomas
 ; APPLICANT: WHITEWAY, Malcolm
 ; APPLICANT: THOMAS, David Y.
 ; TITLE OF INVENTION: THE G-PROTEIN BETA SUBUNIT INTERACTION DOMAIN OF
 ; TITLE OF INVENTION: STE20P/PAK FAMILY OF PROTEIN KINASES AND USES THEREOF
 ; TITLE OF INVENTION: IN BIOASSAYS
 ; FILE REFERENCE: 00122199
 ; CURRENT APPLICATION NUMBER: US/09/226,248B
 ; CURRENT FILING DATE: 1999-01-07
 ; NUMBER OF SEQ ID NOS: 31
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
; NAME/KEY: VARIANT
; LOCATION: (4)
; OTHER INFORMATION: Xaa = A, I, L, M, S, T
; NAME/KEY: VARIANT
; LOCATION: (7)
; OTHER INFORMATION: Xaa = I, V
; NAME/KEY: VARIANT
; LOCATION: (8)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: VARIANT
; LOCATION: (9)..(10)
; OTHER INFORMATION: Xaa = A, I, L, M, S, T
US-09-226-248B-27
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      8 SSL 10
        |||
Db      1 SSL 3
```

RESULT 19

```
US-09-966-871-31
; Sequence 31, Application US/09966871
; Patent No. US20020127539A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; TITLE OF INVENTION: Assays for Identifying Receptors Having
; TITLE OF INVENTION: Alterations in Signaling
; FILE REFERENCE: 00398/512002
; CURRENT APPLICATION NUMBER: US/09/966,871
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,302
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/288,644
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-871-31
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      1 AKS 3
        |||
Db      5 AKS 7
```

RESULT 20

US-09-848-664-6

; Sequence 6, Application US/09848664

; Patent No. US20020146414A1

; GENERAL INFORMATION:

; APPLICANT: Sakiyama-Elbert, Shelly E.

; APPLICANT: Hubbell, Jeffrey A.

; TITLE OF INVENTION: Controlled Release of No. US20020146414A1-Heparin Binding Growth

; TITLE OF INVENTION: Factors from Heparin Containing Matrices

; FILE REFERENCE: ETH 108

; CURRENT APPLICATION NUMBER: US/09/848,664

; CURRENT FILING DATE: 2001-05-03

; PRIOR APPLICATION NUMBER: 09/298,084

; PRIOR FILING DATE: 1999-04-22

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-848-664-6

Query Match 27.3%; Score 3; DB 9; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5

|||

Db 4 SRK 6

RESULT 21

US-09-071-838-286

; Sequence 286, Application US/09071838

; Patent No. US20020152501A1

; GENERAL INFORMATION:

; APPLICANT: Fischer, Robert L.

; APPLICANT: Ohad, Nir

; APPLICANT: Kiyosue, Tomohiro

; APPLICANT: Yadegari, Ramin

; APPLICANT: Margossian, Linda

; APPLICANT: Harada, John

; APPLICANT: Goldberg, Robert B.

; TITLE OF INVENTION: Nucleic Acids That Control Seed and

; TITLE OF INVENTION: Fruit Development in Plants

; NUMBER OF SEQUENCES: 324

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

```

;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/071,838
;     FILING DATE:  01-MAY-1998
;     CLASSIFICATION:  800
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Bastian, Kevin L.
;     REGISTRATION NUMBER:  34,774
;     REFERENCE/DOCKET NUMBER:  023070-086100US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 576-0200
;     TELEFAX:  (415) 576-0300
;   INFORMATION FOR SEQ ID NO:  286:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-09-071-838-286

```

```

Query Match          27.3%;  Score 3;  DB 9;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.1e+04;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy      9 SLM 11
        |||
Db      1 SLM 3

```

RESULT 22

```

US-09-968-561A-298
; Sequence 298, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different
Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 298
; LENGTH: 11

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-298

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 8 SSL 10

RESULT 23

US-09-969-244-11

; Sequence 11, Application US/09969244
; Patent No. US20020173451A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Yao, Siu-Long
; APPLICANT: Jones, Raymond E.
; APPLICANT: Defeo-Jones, Deborah
; APPLICANT: Heimbrook, David C.
; APPLICANT: Rhymer, Patricia A.
; APPLICANT: Wasserbly, Pamela J.
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 20665
; CURRENT APPLICATION NUMBER: US/09/969,244
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/242,815
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(1)
; OTHER INFORMATION: acetylated N-terminus amino acid
US-09-969-244-11

Query Match 27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 9 SSL 11

RESULT 24

US-09-969-244-18

; Sequence 18, Application US/09969244
; Patent No. US20020173451A1


```

; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Yao, Siu-Long
; APPLICANT: Jones, Raymond E.
; APPLICANT: Defeo-Jones, Deborah
; APPLICANT: Heimbrook, David C.
; APPLICANT: Rhymer, Patricia A.
; APPLICANT: Wasserbly, Pamela J.
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 20665
; CURRENT APPLICATION NUMBER: US/09/969,244
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/242,815
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
; NAME/KEY: AMIDATION
; LOCATION: (11)...(11)
; OTHER INFORMATION: leucinamide
US-09-969-244-18

```

```

Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      8 SSL 10
      |||
Db      9 SSL 11

```

RESULT 25

US-09-757-774-13

```

; Sequence 13, Application US/09757774
; Publication No. US20020187156A1
; GENERAL INFORMATION:
; APPLICANT: Dintzis, Howard M.
; APPLICANT: Dintzis, Renee
; APPLICANT: Blodgett, James
; APPLICANT: Cheronis, John
; TITLE OF INVENTION: THERAPEUTIC SUPPRESSION OF SPECIFIC IMMUNE RESPONSES BY
; TITLE OF INVENTION: ADMINISTRATION OF OLIGOMERIC FORMS OF ANTIGEN OF
CONTROLLED
; TITLE OF INVENTION: CHEMISTRY
; FILE REFERENCE: 07265/124004
; CURRENT APPLICATION NUMBER: US/09/757,774
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 08/440,322
; PRIOR FILING DATE: 1995-05-12
; PRIOR APPLICATION NUMBER: US 07/808,797
; PRIOR FILING DATE: 1991-12-17
; PRIOR APPLICATION NUMBER: US 07/628,858

```

```
; PRIOR FILING DATE: 1990-12-17
; PRIOR APPLICATION NUMBER: US 07/354,710
; PRIOR FILING DATE: 1989-05-22
; PRIOR APPLICATION NUMBER: US 07/248,293
; PRIOR FILING DATE: 1988-09-21
; PRIOR APPLICATION NUMBER: US 06/869,808
; PRIOR FILING DATE: 1986-05-29
; PRIOR APPLICATION NUMBER: US 06/460,266
; PRIOR FILING DATE: 1983-01-24
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-757-774-13
```

```
Query Match          27.3%; Score 3; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          1 AKS 3
           .|||
Db          3 AKS 5
```

RESULT 26

```
US-09-999-724-76
; Sequence 76, Application US/09999724
; Publication No. US20030022355A1
; GENERAL INFORMATION:
; APPLICANT: WICKHAM, THOMAS J.
; APPLICANT: KOVESDI, IMRE
; APPLICANT: BROUGH, DOUGLAS E.
; TITLE OF INVENTION: VECTORS AND METHODS FOR GENE TRANSFER
; FILE REFERENCE: 212960
; CURRENT APPLICATION NUMBER: US/09/999,724
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/101,751
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: WO 96US19150
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: US 08/700,846
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/701,124
; PRIOR FILING DATE: 1996-08-21
; PRIOR APPLICATION NUMBER: US 08/563,368
; PRIOR FILING DATE: 1995-11-28
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 76
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-09-999-724-76
```

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 1 SRK 3

RESULT 27

US-09-876-904A-369
; Sequence 369, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 369
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Drosophila Suvar
; FEATURE:
; OTHER INFORMATION: (3) 7 gene product involved in
; OTHER INFORMATION: position-effect variegation (932 aas).
US-09-876-904A-369

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 4 SRK 6

RESULT 28

US-09-876-904A-509
; Sequence 509, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND
THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC
PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 509
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Ig/EBP-1 (immunoglobulin
; OTHER INFORMATION: gene enhancer-binding protein).
US-09-876-904A-509

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KSR 4
|||
Db 3 KSR 5

RESULT 29

US-09-774-381-59

; Sequence 59, Application US/09774381
; Publication No. US20030082677A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Pan, Yang
; APPLICANT: Gearing, David P.
; TITLE OF INVENTION: NOVEL EDIRF, MTR-1, LSP-1, TAP-1, AND PA-I MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-107CP2
; CURRENT APPLICATION NUMBER: US/09/774,381
; CURRENT FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 08/941,354
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/010,674
; PRIOR FILING DATE: 1998-01-22
; PRIOR APPLICATION NUMBER: 60/061,149
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/014,347
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: 60/061,159
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/474,151
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 09/004,206
; PRIOR FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 60/061,143
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 09/483,414
; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: 09/213,571
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 08/994,890
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-774-381-59

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RKG 6
|||
Db 7 RKG 9

RESULT 30

US-09-852-910-259

; Sequence 259, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled
Receptor Signaling
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 259
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(11)
; OTHER INFORMATION: G11 library peptide
US-09-852-910-259

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SIM 11
|||
Db 9 SIM 11

RESULT 31

US-09-802-083-14

; Sequence 14, Application US/09802083
; Publication No. US20030119075A1
; GENERAL INFORMATION:
; APPLICANT: Kirchhofer, Daniel K.
; APPLICANT: Lowe, David G.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Anti-Tissue Factor Antibodies with Enhanced
; TITLE OF INVENTION: Anticoagulant Potency
; FILE REFERENCE: P1736R1
; CURRENT APPLICATION NUMBER: US/09/802,083
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 60/189,775
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 28
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-802-083-14

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 3 NSS 5

RESULT 32

US-09-776-191-59

; Sequence 59, Application US/09776191
; Publication No. US20030119168A1
; GENERAL INFORMATION:
; APPLICANT: Edwin L. Madison
; APPLICANT: Edgar O. Ong
; APPLICANT: Jiunn-Chern Yeh
; APPLICANT: Corvas International, Inc.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: TRANSMEMBRANE SERINE PROTEASES, THE ENCODED PROTEINS AND
; TITLE OF INVENTION: METHODS BASED THEREON
; FILE REFERENCE: 24745-1607
; CURRENT APPLICATION NUMBER: US/09/776,191
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/213,124
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/234,840
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/179,982
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 60/183,542
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: 09/657,968
; PRIOR FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 59
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-776-191-59

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 8 SSL 10

RESULT 33

US-09-968-744A-298

; Sequence 298, Application US/09968744A
; Publication No. US20030148372A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different
Ligands
; FILE REFERENCE: 8039/1073
; CURRENT APPLICATION NUMBER: US/09/968,744A
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 298
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-744A-298

Query Match 27.3%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 8 SSL 10

RESULT 34

US-09-795-798-16

; Sequence 16, Application US/09795798

```

; Publication No. US20030207336A1
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,798
; FILING DATE: 28-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/974,899
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-795-798-16

```

```

Query Match          27.3%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      7 NSS 9
      |||
Db      3 NSS 5

```

```

RESULT 35
US-09-969-322-11
; Sequence 11, Application US/09969322
; Publication No. US20030215456A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Yao, Siu-Long
; APPLICANT: Jones, Raymond E.

```



```
; APPLICANT: Defeo-Jones, Deborah
; APPLICANT: Heimbrosk, David C.
; APPLICANT: Rhymer, Patricia A.
; APPLICANT: Wasserbly, Pamela J.
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 20663
; CURRENT APPLICATION NUMBER: US/09/969,322
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/242,847
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: completely synthetic amino acid sequence
; NAME/KEY: ACETYLATION
; LOCATION: (1)...(1)
; OTHER INFORMATION: acetylated N-terminus amino acid
US-09-969-322-11
```

```
Query Match          27.3%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          8 SSL 10
            |||
Db          9 SSL 11
```

RESULT 36

```
US-09-969-322-18
; Sequence 18, Application US/09969322
; Publication No. US20030215456A1
; GENERAL INFORMATION:
; APPLICANT: Merck & Co., Inc.
; APPLICANT: Yao, Siu-Long
; APPLICANT: Jones, Raymond E.
; APPLICANT: Defeo-Jones, Deborah
; APPLICANT: Heimbrosk, David C.
; APPLICANT: Rhymer, Patricia A.
; APPLICANT: Wasserbly, Pamela J.
; TITLE OF INVENTION: A METHOD OF TREATING CANCER
; FILE REFERENCE: 20663
; CURRENT APPLICATION NUMBER: US/09/969,322
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: 60/242,847
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: completely synthetic amino acid sequence
; NAME/KEY: AMIDATION
; LOCATION: (11)...(11)
; OTHER INFORMATION: leucinamide
US-09-969-322-18

Query Match 27.3%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
| | |
Db 9 SSL 11

RESULT 37

US-09-833-245-301
; Sequence 301, Application US/09833245
; Publication No. US20040010134A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546PCT
; CURRENT APPLICATION NUMBER: US/09/833,245
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 301
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-245-301

Query Match 27.3%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
| | |
Db 1 SSL 3

RESULT 38

US-09-968-561A-298
; Sequence 298, Application US/09968561A
; Publication No. US20040038291A2
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands

```
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 298
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-298
```

```
Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy      8 SSL 10
      |||
Db      8 SSL 10
```

RESULT 39

```
US-10-289-456-91
; Sequence 91, Application US/10289456
; Publication No. US20040033211A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin
; APPLICANT: Maurer, Patrick
; APPLICANT: Spohn, Gunther
; TITLE OF INVENTION: Antigen Arrays for Treatment of Bone Disease
; FILE REFERENCE: 1700.0330001
; CURRENT APPLICATION NUMBER: US/10/289,456
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: PCT/IB02/00166
; PRIOR FILING DATE: 2002-01-21
; PRIOR APPLICATION NUMBER: US 10/050,902
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/396,635
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: US 60/331,045
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

; OTHER INFORMATION: RANKL peptide EF loop
US-10-289-456-91

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GNS 8
|||
Db 5 GNS 7

RESULT 40

US-10-417-895A-63

; Sequence 63, Application US/10417895A
; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Cappuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant peptide for third complementarity
; OTHER INFORMATION: determining region of Fv region of an
; OTHER INFORMATION: immunoglobulin

US-10-417-895A-63

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 1 NSS 3

RESULT 41

US-10-417-895A-66

; Sequence 66, Application US/10417895A
; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Cappuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16

; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant peptide for third complementarity
; OTHER INFORMATION: determining region of Fv region of an
; OTHER INFORMATION: immunoglobulin
US-10-417-895A-66

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 1 NSS 3

RESULT 42

US-10-356-824-3

; Sequence 3, Application US/10356824
; Publication No. US20040037823A9
; GENERAL INFORMATION:
; APPLICANT: Shak, Steve
; APPLICANT: Paton, Virginia
; TITLE OF INVENTION: TREATMENT WITH ANTI-ErbB2 ANTIBODIES
; FILE REFERENCE: P1256R1
; CURRENT APPLICATION NUMBER: US/10/356,824
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/208,649
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/069,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-356-824-3

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 3 NSS 5

RESULT 43

US-10-430-685-35

; Sequence 35, Application US/10430685

```
; Publication No. US20040039543A1
; GENERAL INFORMATION:
; APPLICANT: KECK, Peter
; TITLE OF INVENTION: COMPUTER METHOD AND APPARATUS FOR CLASSIFYING OBJECTS
; FILE REFERENCE: 63040-010210
; CURRENT APPLICATION NUMBER: US/10/430,685
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/US01/44000
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/246,196
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-430-685-35
```

```
Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy      3 SRK 5
        |||
Db      2 SRK 4
```

```
RESULT 44
US-10-430-685-37
; Sequence 37, Application US/10430685
; Publication No. US20040039543A1
; GENERAL INFORMATION:
; APPLICANT: KECK, Peter
; TITLE OF INVENTION: COMPUTER METHOD AND APPARATUS FOR CLASSIFYING OBJECTS
; FILE REFERENCE: 63040-010210
; CURRENT APPLICATION NUMBER: US/10/430,685
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/US01/44000
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/246,196
; PRIOR FILING DATE: 2000-11-06
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-430-685-37
```

```
Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy      3 SRK 5
        |||
Db      2 SRK 4
```

RESULT 45

US-10-430-685-39

; Sequence 39, Application US/10430685
 ; Publication No. US20040039543A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KECK, Peter
 ; TITLE OF INVENTION: COMPUTER METHOD AND APPARATUS FOR CLASSIFYING OBJECTS
 ; FILE REFERENCE: 63040-010210
 ; CURRENT APPLICATION NUMBER: US/10/430,685
 ; CURRENT FILING DATE: 2003-05-06
 ; PRIOR APPLICATION NUMBER: PCT/US01/44000
 ; PRIOR FILING DATE: 2001-11-06
 ; PRIOR APPLICATION NUMBER: 60/246,196
 ; PRIOR FILING DATE: 2000-11-06
 ; NUMBER OF SEQ ID NOS: 240
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 39
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-430-685-39

Query Match 27.3%; Score 3; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
 |||
 Db 2 SRK 4

RESULT 46

US-10-600-152-3

; Sequence 3, Application US/10600152
 ; Publication No. US20040037824A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baughman, Sharon A.
 ; APPLICANT: Shak Steven
 ; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
 ; FILE REFERENCE: P1775R1
 ; CURRENT APPLICATION NUMBER: US/10/600,152
 ; CURRENT FILING DATE: 2003-06-20
 ; PRIOR APPLICATION NUMBER: 09/648,067
 ; PRIOR FILING DATE: 2000-08-25
 ; PRIOR APPLICATION NUMBER: US 60/151,018
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: US 60/213,822
 ; PRIOR FILING DATE: 2000-06-23
 ; NUMBER OF SEQ ID NOS: 15
 ; SEQ ID NO 3
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: salvage receptor binding epitope

US-10-600-152-3

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 3 NSS 5

RESULT 47

US-10-609-217-980

; Sequence 980, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 980
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL-1 ANTAGONIST PEPTIDE
US-10-609-217-980

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NSS 9
|||
Db 2 NSS 4

RESULT 48

US-10-398-104-179

; Sequence 179, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan


```
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-179
```

```
Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

```
Qy      8 SSL 10
        |||
Db      2 SSL 4
```

RESULT 49

```
US-10-458-860-31
; Sequence 31, Application US/10458860
; Publication No. US20040049800A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Rapid Methods For Assessing Therapeutic
; TITLE OF INVENTION: Activity Using Animals Expressing Constitutively Active
G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: 00398/517002
; CURRENT APPLICATION NUMBER: US/10/458,860
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US 60/388,450
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic fragment
US-10-458-860-31
```

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Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;
```

Qy 1 AKS 3
 | | |
Db 5 AKS 7

RESULT 50

US-10-149-135-15

; Sequence 15, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-15

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
 | | |
Db 2 SRK 4

RESULT 51

US-10-149-135-59

; Sequence 59, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide

US-10-149-135-59

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
| | |
Db 2 SRK 4

RESULT 52

US-10-149-135-83

; Sequence 83, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John

```

; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-83

```

```

Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      3 SRK 5
      |||
Db      4 SRK 6

```

```

RESULT 53
US-10-149-135-217
; Sequence 217, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001

```

```

; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 217
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-217

```

```

Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 SRK 5
      |||
Db      5 SRK 7

```

RESULT 54

US-10-149-135-278

```

; Sequence 278, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702

```

; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 278
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-278

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 4 SRK 6

RESULT 55

US-10-149-135-406

; Sequence 406, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04

; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 406
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-406

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 5 SSL 7

RESULT 56

US-10-149-135-409

; Sequence 409, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 409
; LENGTH: 11
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-409

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
| | |
Db 9 SSL 11

RESULT 57

US-10-149-135-414
; Sequence 414, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 414
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-414

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 5 SRK 7

RESULT 58

US-10-149-135-469

; Sequence 469, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 469
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-469

Query Match 27.3%; Score 3; DB 12; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 9 SRK 11

RESULT 59

US-10-149-135-506

```
; Sequence 506, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 506
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-506
```

```
Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      3 SRK 5
        |||
Db      9 SRK 11
```

RESULT 60

US-10-149-135-699

```
; Sequence 699, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
```

```

; APPLICANT:  Sidney, John
; APPLICANT:  Southwood, Scott
; APPLICANT:  Chesnut, Robert
; APPLICANT:  Celis, Esteban
; APPLICANT:  Keogh, Elissa
; TITLE OF INVENTION:  Inducing Cellular Immune Responses to
; TITLE OF INVENTION:  MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE:  2060.0130001
; CURRENT APPLICATION NUMBER:  US/10/149,135
; CURRENT FILING DATE:  2000-12-11
; PRIOR APPLICATION NUMBER:  PCT/US00/33545
; PRIOR FILING DATE:  2000-12-11
; PRIOR APPLICATION NUMBER:  US 09/458,298
; PRIOR FILING DATE:  1999-12-10
; PRIOR APPLICATION NUMBER:  US 09/189,702
; PRIOR FILING DATE:  1998-11-10
; PRIOR APPLICATION NUMBER:  US 08/205,713
; PRIOR FILING DATE:  1994-03-04
; PRIOR APPLICATION NUMBER:  US 08/159,184
; PRIOR FILING DATE:  1993-11-29
; PRIOR APPLICATION NUMBER:  US 08/073,205
; PRIOR FILING DATE:  1993-06-04
; PRIOR APPLICATION NUMBER:  US 08/027,146
; PRIOR FILING DATE:  1993-03-05
; NUMBER OF SEQ ID NOS:  2479
; SOFTWARE:  PatentIn version 3.1
; SEQ ID NO 699
;   LENGTH:  11
;   TYPE:  PRT
;   ORGANISM:  Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION:  Artificial Peptide
US-10-149-135-699

```

```

Query Match          27.3%;  Score 3;  DB 12;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.1e+04;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          8 SSL 10
            |||
Db          7 SSL 9

```

```

RESULT 61
US-10-149-135-738
; Sequence 738, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT:  Fikes, John
; APPLICANT:  Sette, Alessandro
; APPLICANT:  Sidney, John
; APPLICANT:  Southwood, Scott
; APPLICANT:  Chesnut, Robert
; APPLICANT:  Celis, Esteban
; APPLICANT:  Keogh, Elissa
; TITLE OF INVENTION:  Inducing Cellular Immune Responses to
; TITLE OF INVENTION:  MAGE2/3 Using Peptide and Nucleic Acid Compositions

```

; FILE REFERENCE: 2060.0130001
 ; CURRENT APPLICATION NUMBER: US/10/149,135
 ; CURRENT FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/33545
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: US 09/458,298
 ; PRIOR FILING DATE: 1999-12-10
 ; PRIOR APPLICATION NUMBER: US 09/189,702
 ; PRIOR FILING DATE: 1998-11-10
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/159,184
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/073,205
 ; PRIOR FILING DATE: 1993-06-04
 ; PRIOR APPLICATION NUMBER: US 08/027,146
 ; PRIOR FILING DATE: 1993-03-05
 ; NUMBER OF SEQ ID NOS: 2479
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 738
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial Peptide
 US-10-149-135-738

Query Match 27.3%; Score 3; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 9 SSL 11

RESULT 62

US-10-149-135-843

; Sequence 843, Application US/10149135
 ; Publication No. US20040053822A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Keogh, Elissa
 ; TITLE OF INVENTION: Inducing Cellular Immune Responses to
 ; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
 ; FILE REFERENCE: 2060.0130001
 ; CURRENT APPLICATION NUMBER: US/10/149,135
 ; CURRENT FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/33545
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: US 09/458,298
 ; PRIOR FILING DATE: 1999-12-10

; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 843
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-843

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 9 SSL 11

RESULT 63

US-10-149-135-878
; Sequence 878, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205

; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 878
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-878

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 1 SRK 3

RESULT 64

US-10-149-135-903

; Sequence 903, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 903
; LENGTH: 11

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-903

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 5 SSL 7

RESULT 65

US-10-149-135-905
; Sequence 905, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 905
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-905

Query Match 27.3%; Score 3; DB 12; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 1 SRK 3

RESULT 66

US-10-149-135-912

; Sequence 912, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 912
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-912

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 4 SRK 6

RESULT 67

US-10-149-135-948

; Sequence 948, Application US/10149135
 ; Publication No. US20040053822A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Keogh, Elissa
 ; TITLE OF INVENTION: Inducing Cellular Immune Responses to
 ; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
 ; FILE REFERENCE: 2060.0130001
 ; CURRENT APPLICATION NUMBER: US/10/149,135
 ; CURRENT FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/33545
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: US 09/458,298
 ; PRIOR FILING DATE: 1999-12-10
 ; PRIOR APPLICATION NUMBER: US 09/189,702
 ; PRIOR FILING DATE: 1998-11-10
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/159,184
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/073,205
 ; PRIOR FILING DATE: 1993-06-04
 ; PRIOR APPLICATION NUMBER: US 08/027,146
 ; PRIOR FILING DATE: 1993-03-05
 ; NUMBER OF SEQ ID NOS: 2479
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 948
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial Peptide
 US-10-149-135-948

Query Match 27.3%; Score 3; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
 |||
 Db 2 SRK 4

RESULT 68

US-10-149-135-961

; Sequence 961, Application US/10149135
 ; Publication No. US20040053822A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John

```

; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 961
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-961

```

```

Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      3 SRK 5
      |||
Db      5 SRK 7

```

```

RESULT 69
US-10-149-135-991
; Sequence 991, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to

```

```

; TITLE OF INVENTION:  MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE:  2060.0130001
; CURRENT APPLICATION NUMBER:  US/10/149,135
; CURRENT FILING DATE:  2000-12-11
; PRIOR APPLICATION NUMBER:  PCT/US00/33545
; PRIOR FILING DATE:  2000-12-11
; PRIOR APPLICATION NUMBER:  US 09/458,298
; PRIOR FILING DATE:  1999-12-10
; PRIOR APPLICATION NUMBER:  US 09/189,702
; PRIOR FILING DATE:  1998-11-10
; PRIOR APPLICATION NUMBER:  US 08/205,713
; PRIOR FILING DATE:  1994-03-04
; PRIOR APPLICATION NUMBER:  US 08/159,184
; PRIOR FILING DATE:  1993-11-29
; PRIOR APPLICATION NUMBER:  US 08/073,205
; PRIOR FILING DATE:  1993-06-04
; PRIOR APPLICATION NUMBER:  US 08/027,146
; PRIOR FILING DATE:  1993-03-05
; NUMBER OF SEQ ID NOS:  2479
; SOFTWARE:  PatentIn version 3.1
; SEQ ID NO 991
; LENGTH:  11
; TYPE:  PRT
; ORGANISM:  Artificial Sequence
; FEATURE:
; OTHER INFORMATION:  Artificial Peptide
US-10-149-135-991

```

```

Query Match          27.3%;  Score 3;  DB 12;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 1.1e+04;
Matches      3;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

```

```

Qy          3 SRK 5
            |||
Db          4 SRK 6

```

RESULT 70

```

US-10-149-135-999
; Sequence 999, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT:  Fikes, John
; APPLICANT:  Sette, Alessandro
; APPLICANT:  Sidney, John
; APPLICANT:  Southwood, Scott
; APPLICANT:  Chesnut, Robert
; APPLICANT:  Celis, Esteban
; APPLICANT:  Keogh, Elissa
; TITLE OF INVENTION:  Inducing Cellular Immune Responses to
; TITLE OF INVENTION:  MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE:  2060.0130001
; CURRENT APPLICATION NUMBER:  US/10/149,135
; CURRENT FILING DATE:  2000-12-11
; PRIOR APPLICATION NUMBER:  PCT/US00/33545
; PRIOR FILING DATE:  2000-12-11
; PRIOR APPLICATION NUMBER:  US 09/458,298

```

```

; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 999
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Peptide
US-10-149-135-999

```

```

Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative    0; Mismatches    0; Indels      0; Gaps      0;

```

```

Qy      8 SSL 10
      |||
Db      3 SSL 5

```

RESULT 71

```

US-10-149-135-1018
; Sequence 1018, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29

```

```
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1018
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1018
```

```
Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      8 SSL 10
        |||
Db      6 SSL 8
```

RESULT 72

US-10-149-135-1020

```
; Sequence 1020, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1020
```

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1020

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 3 SSL 5

RESULT 73

US-10-149-135-1041

; Sequence 1041, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1041
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1041

Query Match 27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 2 SRK 4

RESULT 74

US-10-149-135-1049

; Sequence 1049, Application US/10149135

; Publication No. US20040053822A1

; GENERAL INFORMATION:

; APPLICANT: Fikes, John

; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott

; APPLICANT: Chesnut, Robert

; APPLICANT: Celis, Esteban

; APPLICANT: Keogh, Elissa

; TITLE OF INVENTION: Inducing Cellular Immune Responses to

; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions

; FILE REFERENCE: 2060.0130001

; CURRENT APPLICATION NUMBER: US/10/149,135

; CURRENT FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: PCT/US00/33545

; PRIOR FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: US 09/458,298

; PRIOR FILING DATE: 1999-12-10

; PRIOR APPLICATION NUMBER: US 09/189,702

; PRIOR FILING DATE: 1998-11-10

; PRIOR APPLICATION NUMBER: US 08/205,713

; PRIOR FILING DATE: 1994-03-04

; PRIOR APPLICATION NUMBER: US 08/159,184

; PRIOR FILING DATE: 1993-11-29

; PRIOR APPLICATION NUMBER: US 08/073,205

; PRIOR FILING DATE: 1993-06-04

; PRIOR APPLICATION NUMBER: US 08/027,146

; PRIOR FILING DATE: 1993-03-05

; NUMBER OF SEQ ID NOS: 2479

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1049

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Artificial Peptide

US-10-149-135-1049

Query Match 27.3%; Score 3; DB 12; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SRK 5
|||
Db 5 SRK 7

RESULT 75

US-10-149-135-1057

```
; Sequence 1057, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1057
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-1057
```

```
Query Match          27.3%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches      3; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
```

```
Qy          8 SSL 10
            |||
Db          1 SSL 3
```

Search completed: April 8, 2004, 16:35:50
Job time : 31.3077 secs

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OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 27.7692 Seconds
(without alignments)
124.984 Million cell updates/sec

Title: US-09-787-443A-21
Perfect score: 11
Sequence: 1 AKSRKGNSSLM 11

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 460

Minimum DB seq length: 11
Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8
Result Query
No. Score Match Length DB ID Description

1	3	27.3	11	2	Q9R872	Q9r872	escherichia
2	3	27.3	11	5	Q9BJ61	Q9bj61	dictyosteli
3	3	27.3	11	8	Q9G622	Q9g622	salea horsf
4	3	27.3	11	8	Q9G616	Q9g616	ceratophora
5	3	27.3	11	8	Q9G610	Q9g610	lyriocephal
6	3	27.3	11	8	Q9G619	Q9g619	ceratophora
7	3	27.3	11	8	Q8WER7	Q8wer7	ceratophora
8	3	27.3	11	8	Q8WD50	Q8wd50	ceratophora
9	3	27.3	11	8	Q9G613	Q9g613	cophotis ce
10	3	27.3	11	8	Q9G5Z5	Q9g5z5	japalura sp
11	3	27.3	11	8	Q8WER4	Q8wer4	ceratophora
12	2	18.2	11	2	Q9R790	Q9r790	borrelia ga
13	2	18.2	11	2	Q47602	Q47602	escherichia
14	2	18.2	11	2	P77404	P77404	escherichia
15	2	18.2	11	2	Q9EUZ3	Q9euz3	escherichia
16	2	18.2	11	2	Q47600	Q47600	escherichia
17	2	18.2	11	2	Q8RMI8	Q8rmi8	enterococcu
18	2	18.2	11	2	P71228	P71228	escherichia
19	2	18.2	11	2	P95518	P95518	pasteurella
20	2	18.2	11	2	Q47345	Q47345	escherichia
21	2	18.2	11	2	Q47420	Q47420	escherichia
22	2	18.2	11	2	Q56413	Q56413	escherichia
23	2	18.2	11	2	Q9R446	Q9r446	neisseria g
24	2	18.2	11	4	Q14759	Q14759	homo sapien
25	2	18.2	11	4	Q9UCP2	Q9ucp2	homo sapien
26	2	18.2	11	4	Q9Y3G2	Q9y3g2	homo sapien
27	2	18.2	11	4	Q16427	Q16427	homo sapien
28	2	18.2	11	4	O75811	O75811	homo sapien
29	2	18.2	11	4	O94785	O94785	homo sapien
30	2	18.2	11	4	Q16234	Q16234	homo sapien
31	2	18.2	11	4	Q8NI03	Q8ni03	homo sapien
32	2	18.2	11	4	Q8TDA8	Q8tda8	homo sapien
33	2	18.2	11	5	Q9UAR8	Q9uar8	aedes aegyp
34	2	18.2	11	5	Q26092	Q26092	pisaster oc
35	2	18.2	11	5	Q9TWX6	Q9twx6	manduca sex
36	2	18.2	11	5	Q99292	Q99292	drosophila
37	2	18.2	11	5	Q25916	Q25916	plasmodium
38	2	18.2	11	5	Q9NFX0	Q9nfx0	drosophila
39	2	18.2	11	5	Q8MPQ3	Q8mpq3	caenorhabdi
40	2	18.2	11	5	P82698	P82698	leucophaea
41	2	18.2	11	5	P82699	P82699	leucophaea
42	2	18.2	11	5	P82700	P82700	leucophaea
43	2	18.2	11	6	Q9XSP7	Q9xsp7	pygathrix n
44	2	18.2	11	6	Q9XSP2	Q9xsp2	hylobates s
45	2	18.2	11	6	Q9TRX2	Q9trx2	bos taurus
46	2	18.2	11	6	Q9XSP5	Q9xsp5	pan troglod
47	2	18.2	11	6	Q9XSP8	Q9xsp8	presbytis j
48	2	18.2	11	6	Q9XSP6	Q9xsp6	pongo pygma
49	2	18.2	11	6	Q9XSQ4	Q9xsq4	gorilla gor
50	2	18.2	11	7	O77900	O77900	oreochromis
51	2	18.2	11	7	O77917	O77917	oreochromis
52	2	18.2	11	7	O77902	O77902	oreochromis
53	2	18.2	11	7	O77921	O77921	pseudotroph
54	2	18.2	11	7	Q9TQB3	Q9tqb3	homo sapien
55	2	18.2	11	7	O77901	O77901	oreochromis
56	2	18.2	11	7	O77892	O77892	oreochromis
57	2	18.2	11	7	O77916	O77916	oreochromis

58	2	18.2	11	7	077885	077885 oreochromis
59	2	18.2	11	7	077905	077905 oreochromis
60	2	18.2	11	7	077884	077884 oreochromis
61	2	18.2	11	7	077906	077906 oreochromis
62	2	18.2	11	7	077899	077899 oreochromis
63	2	18.2	11	7	077918	077918 pseudotroph
64	2	18.2	11	7	077893	077893 oreochromis
65	2	18.2	11	7	078121	078121 oreochromis
66	2	18.2	11	7	077904	077904 oreochromis
67	2	18.2	11	7	077903	077903 oreochromis
68	2	18.2	11	7	077913	077913 oreochromis
69	2	18.2	11	8	Q9G5Y6	Q9g5y6 agama agama
70	2	18.2	11	8	Q8MEL7	Q8mel7 sida hooker
71	2	18.2	11	8	Q9G5Y0	Q9g5y0 pseudotrape
72	2	18.2	11	8	Q8MEM2	Q8mem2 lagunaria p
73	2	18.2	11	8	Q8MES5	Q8mes5 abelmoschus
74	2	18.2	11	8	Q8WD17	Q8wdl7 ctenophorus
75	2	18.2	11	8	Q9G368	Q9g368 draco blanf
76	2	18.2	11	8	Q8MEP0	Q8mep0 hibiscus pe
77	2	18.2	11	8	Q32704	Q32704 nicotiana t
78	2	18.2	11	8	Q8MES1	Q8mes1 alyogyne pi
79	2	18.2	11	8	Q8MEP3	Q8mep3 hibiscus no
80	2	18.2	11	8	Q8MEQ7	Q8meq7 hibiscus dr
81	2	18.2	11	8	Q35374	Q35374 paramecium
82	2	18.2	11	8	Q8MEL9	Q8mel9 pavonia has
83	2	18.2	11	8	Q8MER0	Q8mer0 hibiscus co
84	2	18.2	11	8	Q8MES3	Q8mes3 alyogyne cr
85	2	18.2	11	8	Q9G658	Q9g658 hydrosaurus
86	2	18.2	11	8	Q34380	Q34380 drosophila
87	2	18.2	11	8	Q8MEP5	Q8mep5 hibiscus mi
88	2	18.2	11	8	Q8MER1	Q8mer1 hibiscus ca
89	2	18.2	11	8	Q8MER7	Q8mer7 fioria viti
90	2	18.2	11	8	Q9G5Y3	Q9g5y3 agama impal
91	2	18.2	11	9	Q37925	Q37925 bacterioph
92	2	18.2	11	10	Q9S8Z8	Q9s8z8 psophocarpu
93	2	18.2	11	10	O65901	O65901 leavenworth
94	2	18.2	11	10	Q8RV30	Q8rv30 zea mays (m
95	2	18.2	11	10	Q39784	Q39784 gossypium h
96	2	18.2	11	10	O82070	O82070 triticum ae
97	2	18.2	11	10	Q94IR5	Q94ir5 pinus radia
98	2	18.2	11	10	Q04131	Q04131 lycopersico
99	2	18.2	11	10	P82436	P82436 nicotiana t
100	2	18.2	11	10	Q7X9Y3	Q7x9y3 cucumis sat

ALIGNMENTS

RESULT 1

Q9R872

ID Q9R872 PRELIMINARY; PRT; 11 AA.

AC Q9R872;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Dihydrofolate reductase (Fragment).

GN DFR1.

OS Escherichia coli.
 OG Plasmid r483.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Tn7;
 RA Hansson K., Sundstrom L., Pelletier A., Roy P.H.;
 RT "Sequence and function of the second type of integron in Tn7.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Tn7;
 RX MEDLINE=82220022; PubMed=6283361;
 RA Lichtenstein C., Brenner S.;
 RT "Unique insertion site of Tn7 in the E. coli chromosome.";
 RL Nature 297:601-603(1982).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Tn7;
 RX MEDLINE=83290694; PubMed=6411680;
 RA Simonsen C.C., Chen E.Y., Levinson A.D.;
 RT "Identification of the type I trimethoprim-resistant dihydrofolate
 RT reductase specified by the Escherichia coli R-plasmid R483: Comparison
 RT with procaryotic and eucaryotic dihydrofolate reductases.";
 RL J. Bacteriol. 155:1001-1008(1983).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Tn7;
 RX MEDLINE=83272957; PubMed=6308574;
 RA Fling M.E., Richards C.;
 RT "The nucleotide sequence of the trimethoprim-resistant dihydrofolate
 RT reductase gene harbored by Tn7.";
 RL Nucleic Acids Res. 11:5147-5158(1983).
 DR EMBL; AJ001816; CAA05032.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Plasmid.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1221 MW; 92014864C2C69735 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SLM 11
 |||
 Db 4 SLM 6

RESULT 2

Q9BJ61

ID Q9BJ61 PRELIMINARY; PRT; 11 AA.
 AC Q9BJ61;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE G-box binding factor (Fragment).
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21290831; PubMed=11397018;
 RA Brown J.M., Firtel R.A.;
 RT "Functional and regulatory analysis of the Dictyostelium G-box binding
 RT factor.";
 RL Dev. Biol. 234:521-534(2001).
 DR EMBL; AF337815; AAK21290.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1248 MW; 87356B5FD1E1E1F1 CRC64;

Query Match 27.3%; Score 3; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GNS 8
 |||
 Db 9 GNS 11

RESULT 3

Q9G622

ID Q9G622 PRELIMINARY; PRT; 11 AA.
 AC Q9G622;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Salea horsfieldii.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Salea.
 OX NCBI_TaxID=118233;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128490; AAG00707.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.

FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 2 SSL 4

RESULT 4

Q9G616

ID Q9G616 PRELIMINARY; PRT; 11 AA.

AC Q9G616;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Cytochrome c oxidase subunit I (Fragment).

GN COI.

OS Ceratophora stoddartii.

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;

OC Ceratophora.

OX NCBI_TaxID=118196;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22114082; PubMed=12118408;

RA Macey J.R., Schulte J.A. II, Larson A.;

RT "Evolution and information content of the mitochondrial genomic
structural features illustrated with acrodont lizards.";

RL Syst. Biol. 49:257-277(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22114081; PubMed=12118407;

RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,

RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;

RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
phylogenetics.";

RL Syst. Biol. 49:233-256(2000).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=21655505; PubMed=11796034;

RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;

RT "Rostral Horn Evolution among Agamid Lizards of the Genus Ceratophora
Endemic to Sri Lanka.";

RL Mol. Phylogenet. Evol. 22:111-117(2002).

DR EMBL; AF128492; AAG00713.1; -.

DR EMBL; AF364054; AAL68027.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1295 MW; 5B2C371E336411A7 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 2 SSL 4

RESULT 5

Q9G610

ID Q9G610 PRELIMINARY; PRT; 11 AA.
AC Q9G610;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Lyriocephalus scutatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Lyriocephalus.
OX NCBI_TaxID=118218;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21655505; PubMed=11796034;
RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;
RT "Rostral Horn Evolution among Agamid Lizards of the Genus Ceratophora
RT Endemic to Sri Lanka.";
RL Mol. Phylogenet. Evol. 22:111-117(2002).
DR EMBL; AF128494; AAG00719.1; -.
DR EMBL; AF364052; AAL68021.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1295 MW; 5B2C371E336411A7 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10

Db |||
 2 SSL 4

RESULT 6

Q9G619

ID Q9G619 PRELIMINARY; PRT; 11 AA.
AC Q9G619;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Ceratophora aspera.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Ceratophora.
OX NCBI_TaxID=118195;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128491; AAG00710.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
Db 2 SSL 4

RESULT 7

Q8WER7

ID Q8WER7 PRELIMINARY; PRT; 11 AA.
AC Q8WER7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).

GN COI.
 OS Ceratophora tennentii.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Ceratophora.
 OX NCBI_TaxID=118087;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and phylogenetic information content of mitochondrial
 RT genomic structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21655505; PubMed=11796034;
 RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;
 RT "Rostral Horn Evolution among Agamid Lizards of the Genus Ceratophora
 RT Endemic to Sri Lanka.";
 RL Mol. Phylogenet. Evol. 22:111-117(2002).
 DR EMBL; AF128521; AAL67607.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 2 SSL 4

RESULT 8

Q8WD50

ID Q8WD50 PRELIMINARY; PRT; 11 AA.
 AC Q8WD50;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Ceratophora stoddartii.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Ceratophora.
 OX NCBI_TaxID=118196;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21655505; PubMed=11796034;
 RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;
 RT "Rostral Horn Evolution among Agamid Lizards of the Genus Ceratophora
 RT Endemic to Sri Lanka.";

RL Mol. Phylogenet. Evol. 22:111-117(2002).
DR EMBL; AF364053; AAL68024.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
|||
Db 2 SSL 4

RESULT 9

Q9G613

ID Q9G613 PRELIMINARY; PRT; 11 AA.
AC Q9G613;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Cophotis ceylanica.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Cophotis.
OX NCBI_TaxID=118202;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128493; AAG00716.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1295 MW; 5B2C371E336411A7 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10

Db |||
 2 SSL 4

RESULT 10

Q9G5Z5

ID Q9G5Z5 PRELIMINARY; PRT; 11 AA.
AC Q9G5Z5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Japalura splendida.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
OC Japalura.
OX NCBI_TaxID=118209;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114082; PubMed=12118408;
RA Macey J.R., Schulte J.A. II, Larson A.;
RT "Evolution and information content of the mitochondrial genomic
RT structural features illustrated with acrodont lizards.";
RL Syst. Biol. 49:257-277(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22114081; PubMed=12118407;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
RT phylogenetics.";
RL Syst. Biol. 49:233-256(2000).
DR EMBL; AF128501; AAG00740.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1295 MW; 5B2C371E336411A7 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
Db 2 SSL 4

RESULT 11

Q8WER4

ID Q8WER4 PRELIMINARY; PRT; 11 AA.
AC Q8WER4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).

GN COI.
 OS Ceratophora erdeleni.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Ceratophora.
 OX NCBI_TaxID=118085;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and phylogenetic information content of mitochondrial
 RT genomic structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21655505; PubMed=11796034;
 RA Schulte J.A. II, Macey J.R., Pethiyagoda R., Larson A.;
 RT "Rostral Horn Evolution among Agamid Lizards of the Genus Ceratophora
 RT Endemic to Sri Lanka.";
 RL Mol. Phylogenet. Evol. 22:111-117(2002).
 DR EMBL; AF128522; AAL67610.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1264 MW; 5B2C371E33640DD7 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 9.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SSL 10
 |||
 Db 2 SSL 4

RESULT 12

Q9R790

ID Q9R790 PRELIMINARY; PRT; 11 AA.
 AC Q9R790;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Outer surface protein C (Fragment).
 GN OSPC.
 OS Borrelia garinii.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=29519;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G25;
 RX MEDLINE=97426044; PubMed=9282748;
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 RA Rosa P.;
 RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
 RT plasmid structure and targeted inactivation of the ospC gene.";
 RL Mol. Microbiol. 25:361-374(1997).

DR EMBL; U93700; AAC45535.1; -.
 DR GO; GO:0009279; C:external outer membrane (sensu Gram-negativ. . .; IEA.
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR InterPro; IPR001800; Lipoprotein_6.
 DR Pfam; PF01441; Lipoprotein_6; 1.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1250 MW; 0868D864C5B731A4 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
 ||
 Db 10 LM 11

RESULT 13

Q47602

ID Q47602 PRELIMINARY; PRT; 11 AA.
 AC Q47602;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE REase protein (Fragment).
 GN REASE.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91139577; PubMed=1995588;
 RA Tao T., Bourne J.C., Blumenthal R.M.;
 RT "A family of regulatory genes associated with type II restriction-
 RT modification systems."
 RL J. Bacteriol. 173:1367-1375(1991).
 DR EMBL; M63620; AAA24558.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1412 MW; 80ABB190C736DAAA CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 2 SR 3

RESULT 14

P77404

ID P77404 PRELIMINARY; PRT; 11 AA.
 AC P77404;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE DNA sequence downstream of the ECOPRRI HSD locus (Fragment).
 GN HSDR.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97206151; PubMed=9157244;
 RA Tyndall C., Lehnherr H., Sandmeier U., Kulik E., Bickle T.A.;
 RT "The type IC hsd loci of the enterobacteria are flanked by DNA with
 RT high homology to the phage P1 genome: implications for the evolution
 RT and spread of DNA restriction systems."
 RL Mol. Microbiol. 23:729-736(1997).
 DR EMBL; X98145; CAA66840.1; -.
 DR EMBL; X98144; CAA66839.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1259 MW; 714AB092A4072734 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KS 3
 ||
 Db 1 KS 2

RESULT 15
 Q9EUZ3

ID Q9EUZ3 PRELIMINARY; PRT; 11 AA.
 AC Q9EUZ3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Ribosome binding factor A (Fragment).
 GN RBFA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IQ490;
 RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,
 RA Mortensen K.K.;
 RT "Sequence of the infB gene from Escherichia coli strain IQ489 and
 RT IQ490."
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ132862; CAC20133.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1319 MW; 6B234CFE740879CB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 2 AK 3

RESULT 16

Q47600

ID Q47600 PRELIMINARY; PRT; 11 AA.
AC Q47600;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE REase protein (Fragment).
GN REASE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
RT modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
DR EMBL; M63619; AAA24556.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1232 MW; 63175479572AB5A4 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
||
Db 2 SL 3

RESULT 17

Q8RMI8

ID Q8RMI8 PRELIMINARY; PRT; 11 AA.
AC Q8RMI8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ErmB (Fragment).
GN ERMB.
OS Enterococcus hirae.
OG Plasmid pMKH1.
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1354;
RN [1]
RP SEQUENCE FROM N.A.
RA Borgen K., Sorum M., Wasteson Y., Kruse H., Oppegaard H.;
RT "Genetic linkage between ermB and vanA in Enterococcus hirae of
RT poultry origin.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF493942; AAM18554.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1359 MW; 08A7A8AA49C7273B CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RK 5
||
Db 10 RK 11

RESULT 18

P71228

ID P71228 PRELIMINARY; PRT; 11 AA.
AC P71228;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Nitrate/nitrite sensor transmitter (Fragment).
GN NARQ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=92374842; PubMed=1508040;
RA Chiang R.C., Cavicchioli R., Gunsalus R.P.;
RT "Identification and characterization of narQ, a second nitrate sensor
RT for nitrate-dependent gene regulation in Escherichia coli.";
RL Mol. Microbiol. 6:1913-1923(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=97113461; PubMed=8955321;
RA Cavicchioli R., Kolesnikow T., Chiang R.C., Gunsalus R.P.;
RT "Characterization of the aegA locus of Escherichia coli: control of
RT gene expression in response to anaerobiosis and nitrate.";
RL J. Bacteriol. 178:6968-6974(1996).
DR EMBL; L34011; AAB46943.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1200 MW; 52E1CFFCA2D77403 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
||
Db 10 SL 11

RESULT 19

P95518

ID P95518 PRELIMINARY; PRT; 11 AA.
 AC P95518;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ribosomal protein RpsA (Fragment).
 GN RPSA.
 OS Pasteurella haemolytica.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Mannheimia.
 OX NCBI_TaxID=75985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PHL101;
 RX MEDLINE=97164347; PubMed=9011038;
 RA Highlander S.K., Garza O., Brown B.J., Koby S., Oppenheim A.B.;
 RT "Isolation and characterization of the integration host factor genes
 RT of Pasteurella haemolytica."
 RL FEMS Microbiol. Lett. 146:181-188(1997).
 DR EMBL; U56139; AAC44845.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 11 AA; 1168 MW; 7A4BFD38D339CDDDB CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 8 AK 9

RESULT 20

Q47345

ID Q47345 PRELIMINARY; PRT; 11 AA.
 AC Q47345;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Leader peptide.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Faber F., van Giezen M., Van Gorcom R.F.M., Harder W.;
 RT "Identification of two Escherichia coli K12 proteins which are induced
 RT in response to pollutant stress."
 RL Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE OF 2-11 FROM N.A.
 RC STRAIN=K12;

RX MEDLINE=85134883; PubMed=6396419;
RA Hudson G.S., Davidson B.E.;
RT "Nucleotide sequence and transcription of the phenylalanine and
RT tyrosine operons of Escherichia coli K12.";
RL J. Mol. Biol. 180:1023-1051(1984).
DR EMBL; Z70523; CAA94435.1; -.
SQ SEQUENCE 11 AA; 1402 MW; 87AB199204141775 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NS 8
||
Db 3 NS 4

RESULT 21

Q47420

ID Q47420 PRELIMINARY; PRT; 11 AA.
AC Q47420;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ORF11 protein.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92041688; PubMed=1657895;
RA Sharples G.J., Lloyd R.G.;
RT "Resolution of Holliday junctions in Escherichia coli: Identification
RT of the ruvC gene product as a 19-Kilodalton protein.";
RL J. Bacteriol. 173:7711-7715(1991).
DR EMBL; X59551; CAA42127.1; -.
DR PIR; S19015; S19015.
SQ SEQUENCE 11 AA; 1215 MW; DD8D6D4D56C6D33D CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 4 AK 5

RESULT 22

Q56413

ID Q56413 PRELIMINARY; PRT; 11 AA.
AC Q56413;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE IS602L region DNA, 5' end (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TRANSPOSON=Transposon Tn602;
 RX MEDLINE=87318208; PubMed=2819910;
 RA Stibitz S., Davies J.E.;
 RT "Tn602: A naturally occurring relative of Tn903 with direct repeats.";
 RL Plasmid 17:202-209(1987).
 DR EMBL; M22735; AAA27464.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1361 MW; 447E8354A05339C3 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 1 AK 2

RESULT 23

Q9R446

ID Q9R446 PRELIMINARY; PRT; 11 AA.
 AC Q9R446;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Carbamoyl-phosphate synthase subunit A (Fragment).
 GN CARA.
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11, and FA1090;
 RX MEDLINE=95291461; PubMed=7773412;
 RA Lawson F.S., Billowes F.M., Dillon J.A.;
 RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
 RT gonorrhoeae includes a large, variable intergenic sequence which is
 RT also present in other Neisseria species.";
 RL Microbiology 141:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS11, and FA1090;
 RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
 RT "Complexity of the variable sequence between the carbamoyl-phosphate
 RT synthase genes of Neisseria species.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF029363; AAC78453.1; -.
 DR EMBL; AF029362; AAC78452.1; -.

FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1178 MW; 0C07A8E3DDD33694 CRC64;

Query Match 18.2%; Score 2; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
||
Db 8 AK 9

RESULT 24

Q14759

ID Q14759 PRELIMINARY; PRT; 11 AA.
AC Q14759;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lymphocyte cytosolic protein 2 (Fragment).
GN LCP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sunden S.L.F., Carr L.L., Clements J.L., Motto D.G., Koretzky G.A.;
RT "Polymorphism in and localization of the gene encoding the 76 kDa SH2
RT domain-containing Leukocyte Protein (SLP-76) to chromosome 5q33.1-
RT qter.";
RL Genomics 0:0-0(1995).
DR EMBL; U44065; AAA93308.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1242 MW; D695104224072DDD CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RK 5
||
Db 7 RK 8

RESULT 25

Q9UCP2

ID Q9UCP2 PRELIMINARY; PRT; 11 AA.
AC Q9UCP2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE cGMP-inhibited LOW K(M) cAMP phosphodiesterase PEAK 43, CGI-PDE
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92283180; PubMed=1317779;
 RA LeBon T.R., Kasuya J., Paxton R.J., Belfrage P., Hockman S.,
 RA Manganiello V.C., Fujita Yamaguchi Y.;
 RT "Purification and characterization of guanosine 3',5'-monophosphate-
 RT inhibited low K(m) adenosine 3',5'-monophosphate phosphodiesterase
 RT from human placental cytosolic fractions.";
 RL Endocrinology 130:3265-3274(1992).
 DR GO; GO:0005829; C:cytosol; TAS.
 DR GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
 DR GO; GO:0007165; P:signal transduction; NAS.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1220 MW; 7DF1FDF2D44735BB CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
 ||
 Db 1 SL 2

RESULT 26

Q9Y3G2

ID Q9Y3G2 PRELIMINARY; PRT; 11 AA.
 AC Q9Y3G2;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE LSFR2 protein (Fragment).
 GN LSFR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99299247; PubMed=10369878;
 RA Gilley J., Fried M.;
 RT "Extensive gene order differences within regions of conserved synten
 RT between the Fugu and human genomes: implications for chromosomal
 RT volution and the cloning of disease genes.";
 RL Hum. Mol. Genet. 8:1313-1320(1999).
 DR EMBL; Y17456; CAB44349.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1342 MW; 68C5E5D7A8772324 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RK 5
||
Db 4 RK 5

RESULT 27

Q16427

ID Q16427 PRELIMINARY; PRT; 11 AA.
AC Q16427;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Dystrophin protein (Fragment).
GN DYSTROPHIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163501; PubMed=8566960;
RA Holder E., Maeda M., Bies R.D.;
RT "Expression and regulation of the dystrophin Purkinje promoter in
RT human skeletal muscle, heart, and brain."
RL Hum. Genet. 97:232-239(1996).
DR EMBL; S81419; AAD14362.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1299 MW; DDCC84321AB5A5A2 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 5 SS 6

RESULT 28

O75811

ID O75811 PRELIMINARY; PRT; 11 AA.
AC O75811;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE ErbB-3 R2 (Fragment).
GN C-ERBB-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovarian carcinoma;
RX MEDLINE=98345147; PubMed=9681822;
RA Lee H., Maihle N.J.;
RT "Isolation and characterization of four alternate c-erbB3 transcripts

RT expressed in ovarian carcinoma-derived cell lines and normal human
RT tissues.";
RL Oncogene 16:3243-3252(1998).
DR EMBL; U88358; AAC39858.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1017 MW; 21B236366EB72878 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KG 6
||
Db 9 KG 10

RESULT 29

O94785

ID O94785 PRELIMINARY; PRT; 11 AA.
AC O94785;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Thrombopoietin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki Y., Takahashi T., Nakamura K., Okuno Y., Nakao K.;
RT "Production of Thrombopoietin by Human Carcinomas and Its Novel mRNA
RT Isoforms.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB014683; BAA34932.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1203 MW; 5FE19F44B6C1A877 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
||
Db 2 SL 3

RESULT 30

Q16234

ID Q16234 PRELIMINARY; PRT; 11 AA.
AC Q16234;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE HuD protein (Fragment).
GN HUD.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94349312; PubMed=8069866;
 RA Sekido Y., Bader S.A., Carbone D.P., Johnson B.E., Minna J.D.;
 RT "Molecular analysis of the HuD gene encoding a paraneoplastic
 RT encephalomyelitis antigen in human lung cancer cell lines."
 RL Cancer Res. 54:4988-4992(1994).
 DR EMBL; S73887; AAD14142.1; -.
 DR PIR; I52708; I52708.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1289 MW; 2EDCF20E204415A7 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 5 SR 6

RESULT 31

Q8NI03

ID Q8NI03 PRELIMINARY; PRT; 11 AA.
 AC Q8NI03;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE 25 hydroxyvitamin d3 1-alpha hydroxylase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ebert R., Schneider D., Jovanovic M., Adamski J., Jakob F.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF500480; AAM21669.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1298 MW; 82C14E84CB533731 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 9 SR 10

RESULT 32

Q8TDA8

ID Q8TDA8 PRELIMINARY; PRT; 11 AA.
 AC Q8TDA8;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Glutathione synthetase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cho Y.-W., Lee Y.-Y., Lim C.-J.;
 RT "Cloning and characterization of glutathione synthetase gene from
 RT human placenta DNA.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF485789; AAL91591.1; -.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1235 MW; 1CE28D1E35B86374 CRC64;

Query Match 18.2%; Score 2; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
 ||
 Db 7 SL 8

RESULT 33

Q9UAR8

ID Q9UAR8 PRELIMINARY; PRT; 11 AA.
 AC Q9UAR8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Sialokinin I preproprotein (Fragment).
 OS Aedes aegypti (Yellowfever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
 OX NCBI_TaxID=7159;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rockefeller/Red; TISSUE=Salivary gland;
 RX MEDLINE=20099025; PubMed=10620041;
 RA Beerntsen B.T., Champagne D.E., Coleman J.L., Campos Y.A., James A.A.;
 RT "Characterization of the Sialokinin I gene encoding the salivary
 RT vasodilator of the yellow fever mosquito, Aedes aegypti.";
 RL Insect Mol. Biol. 8:459-467(1999).
 DR EMBL; AF108100; AAD16884.1; -.
 DR GO; GO:0007268; P:synaptic transmission; IEA.
 DR GO; GO:0007217; P:tachykinin signaling pathway; IEA.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 FT NON TER 1 1
 SQ SEQUENCE 11 AA; 1203 MW; 8BADC77C6B59C33A CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 9 LM 10

RESULT 34

Q26092

ID Q26092 PRELIMINARY; PRT; 11 AA.
AC Q26092;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Sea StAR histone H2B gene 5'region (Fragment).
OS Pisaster ochraceus (Sea star).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC Asteroidea; Forcipulatacea; Forcipulatida; Asteriidae; Pisaster.
OX NCBI_TaxID=7612;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sperm;
RA Howell A.M., Cool D., Hewitt J., Ydenberg B., Smith M.J., Honda B.M.;
RT "Organization and Unusual Expression of Histone Genes in the Sea Star
RT Pisaster ochraceus.";
RL J. Mol. Evol. 25:29-36(1987).
DR EMBL; X05619; CAA29106.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1128 MW; 5173974A3865BDD3 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KG 6
||
Db 8 KG 9

RESULT 35

Q9TWX6

ID Q9TWX6 PRELIMINARY; PRT; 11 AA.
AC Q9TWX6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Juvenile hormone binding protein, JHBP=12.5 kDa CNBR peptide
DE (Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE.
RX MEDLINE=92134256; PubMed=1734862;
RA Touhara K., Prestwich G.D.;

RT "Binding site mapping of a photoaffinity-labeled juvenile hormone
 RT binding protein.";
 RL Biochem. Biophys. Res. Commun. 182:466-473(1992).
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2
 ||
 Db 10 AK 11

RESULT 36

Q99292

ID Q99292 PRELIMINARY; PRT; 11 AA.
 AC Q99292;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Bicoid protein (Fragment).
 GN BCD.
 OS Drosophila heteroneura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=32382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91184004; PubMed=2081457;
 RA MacDonald P.M.;
 RT "bicoid mRNA localization signal: phylogenetic conservation of
 RT function and RNA secondary structure.";
 RL Development 110:161-171(1990).
 CC -!- FUNCTION: BICOID IS SEGMENT-POLARITY PROTEIN THAT PROVIDES
 CC POSITIONAL CUES FOR THE DEVELOPMENT OF HEAD AND THORACIC SEGMENTS.
 CC BCD REGULATES THE EXPRESSION OF ZYGOTIC GENES, POSSIBLY THROUGH
 CC ITS HOMEODOMAIN, AND INHIBITS THE ACTIVITY OF OTHER MATERNAL GENE
 CC PRODUCTS. IT IS POSSIBLE THAT BCD ALSO BINDS RNA.
 DR EMBL; M32125; AAA28386.1; -.
 DR FlyBase; FBgn0012352; Dhet\bcd.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR GO; GO:0007367; P:segment polarity determination; IEA.
 KW DNA-binding; Developmental protein; Homeobox; Nuclear protein;
 KW RNA-binding; Segmentation polarity protein; Transcription regulation.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1221 MW; 8CE802305DD9D6C1 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GN 7
||
Db 2 GN 3

RESULT 37

Q25916

ID Q25916 PRELIMINARY; PRT; 11 AA.
AC Q25916;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Malaria antigen (7H8/2) (Fragment).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91164876; PubMed=1706114;
RA Limpiaiboon T., Taylor D., Jones G., Geysen H.M., Saul A.;
RT "Characterization of a Plasmodium falciparum epitope recognized by a
RT monoclonal antibody with broad isolate and species specificity.";
RL Southeast Asian J. Trop. Med. Public Health 21:388-396(1990).
DR EMBL; M31305; AAA29645.1; -.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1415 MW; DB03D3BC42C33699 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KS 3
||
Db 1 KS 2

RESULT 38

Q9NFX0

ID Q9NFX0 PRELIMINARY; PRT; 11 AA.
AC Q9NFX0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Mitochondrial aconitase (Fragment).
GN ACON OR MAC OR CG9244.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON S;
RA Lind M.I.;
RT "Charaterisation of two iron regulatory proteins and mitochondrial

RT aconitase in *Drosophila melanogaster*.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ252019; CAB93522.1; -.
DR FlyBase; FBgn0010100; Acon.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1204 MW; 7C889CE4D4469734 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 5 LM 6

RESULT 39

Q8MPQ3

ID Q8MPQ3 PRELIMINARY; PRT; 11 AA.
AC Q8MPQ3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein Y23H5A.8b.
GN Y23H5A.8.
OS *Caenorhabditis elegans*.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; *Caenorhabditis*.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode *C. elegans*: a platform for
RT investigating biology. The *C. elegans* Sequencing Consortium."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Dempsey S., Le T.T.;
RT "The sequence of *C. elegans* cosmid Y23H5A."
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF077541; AAM54173.1; -.
DR WormPep; Y23H5A.8b; CE31097.
KW Hypothetical protein.
SQ SEQUENCE 11 AA; 1319 MW; 6920D63A21B77414 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 3 SR 4

RESULT 40

P82698

ID P82698 PRELIMINARY; PRT; 11 AA.
AC P82698;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Periviscerokinin-1 (LEM-PVK-1).
OS Leucophaea maderae (Madeira cockroach),
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS Blaberus craniifer,
OS Blaptica dubia, and
OS Gromphadorina portentosa (Cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
RT "Identification of novel periviscerokinins from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation.";
RL Eur. J. Biochem. 267:3869-3873(2000).
CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -!- MASS SPECTROMETRY: MW=1090.6; METHOD=MALDI.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
KW Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1091 MW; 2C2D80E2D7605728 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
||
Db 2 SS 3

RESULT 41

P82699

ID P82699 PRELIMINARY; PRT; 11 AA.
AC P82699;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Periviscerokinin-2 (LEM-PVK-2).
OS Leucophaea maderae (Madeira cockroach),

OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
 OS Blaberus craniifer,
 OS Blaptica dubia, and
 OS Gromphadorina portentosa (Cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
 RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
 RX MEDLINE=20307624; PubMed=10849006;
 RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
 RT "Identification of novel periviscerokinins from single neurohaemal
 RT release sites in insects. MS/MS fragmentation complemented by Edman
 RT degradation.";
 RL Eur. J. Biochem. 267:3869-3873(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -!- MASS SPECTROMETRY: MW=1102.6; METHOD=MALDI.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1103 MW; 2F4D9FFD85B05728 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
 ||
 Db 2 SS 3

RESULT 42

P82700

ID P82700 PRELIMINARY; PRT; 11 AA.
 AC P82700;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Periviscerokinin-3 (LEM-PVK-3).
 OS Leucophaea maderae (Madeira cockroach),
 OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
 OS Blaberus craniifer,
 OS Blaptica dubia (Argentinian wood cockroach), and
 OS Gromphadorina portentosa (Cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
 RC TISSUE=ABDOMINAL PERISYMPATHETIC ORGANS;
 RX MEDLINE=20307624; PubMed=10849006;
 RA Predel R., Kellner R., Baggerman G., Steinmetzer T., Schoofs L.;
 RT "Identification of novel periviscerokinins from single neurohaemal

RT release sites in insects. MS/MS fragmentation complemented by Edman
 RT degradation.";
 RL Eur. J. Biochem. 267:3869-3873(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -!- MASS SPECTROMETRY: MW=1146.6; METHOD=MALDI.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
 KW Neuropeptide; Amidation.
 FT MOD RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1147 MW; 2F4D9FF2D7605698 CRC64;

Query Match 18.2%; Score 2; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 SS 9
 ||
 Db 2 SS 3

RESULT 43

Q9XSP7

ID Q9XSP7 PRELIMINARY; PRT; 11 AA.
 AC Q9XSP7;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain (Fragment).
 GN PDGFA.
 OS Pygathrix nemaeus (Dove langur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 OC Pygathrix.
 OX NCBI_TaxID=54133;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20065871; PubMed=10598812;
 RA Bonthron D.T., Smith S.L., Campbell R.;
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."
 RL Hum. Genet. 105:452-459(1999).
 DR EMBL; AJ243282; CAB45924.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 3 SR 4

RESULT 44

Q9XSP2

ID Q9XSP2 PRELIMINARY; PRT; 11 AA.

AC Q9XSP2;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain (Fragment).
 GN PDGFA.
 OS Hylobates syndactylus (Siamang) (Symphalangus syndactylus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 OX NCBI_TaxID=9590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20065871; PubMed=10598812;
 RA Bonthron D.T., Smith S.L., Campbell R.;
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."
 RL Hum. Genet. 105:452-459(1999).
 DR EMBL; AJ243280; CAB45927.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 3 SR 4

RESULT 45

Q9TRX2

ID Q9TRX2 PRELIMINARY; PRT; 11 AA.
 AC Q9TRX2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Glutamate dehydrogenase (EC 1.4.1.3) (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91308094; PubMed=1854724;
 RA Ozturk D.H., Colman R.F.;
 RT "Identification of cysteine-319 as the target amino acid of 8-[(4-bromo-2,3-dioxobutyl)thio]adenosine 5'-triphosphate in bovine liver glutamate dehydrogenase."
 RL Biochemistry 30:7126-7134(1991).
 DR GO; GO:0004353; F:glutamate dehydrogenase [NAD(P)] activity; IEA.
 SQ SEQUENCE 11 AA; 1207 MW; F46BF756A771B401 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KG 6
||
Db 9 KG 10

RESULT 46

Q9XSP5

ID Q9XSP5 PRELIMINARY; PRT; 11 AA.
AC Q9XSP5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN PDGFA.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus."
RL Hum. Genet. 105:452-459(1999).
DR EMBL; AJ243277; CAB45926.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 3 SR 4

RESULT 47

Q9XSP8

ID Q9XSP8 PRELIMINARY; PRT; 11 AA.
AC Q9XSP8;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Platelet-derived growth factor A chain (Fragment).
GN PDGFA.
OS Presbytis johnii.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Presbytis.
OX NCBI_TaxID=98375;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;

RT "Complex patterns of intragenic polymorphism at the PDGFA locus."
 RL Hum. Genet. 105:452-459(1999).
 DR EMBL; AJ243281; CAB46013.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 3 SR 4

RESULT 48

Q9XSP6

ID Q9XSP6 PRELIMINARY; PRT; 11 AA.
 AC Q9XSP6;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain (Fragment).
 GN PDGFA.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20065871; PubMed=10598812;
 RA Bonthron D.T., Smith S.L., Campbell R.;
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."
 RL Hum. Genet. 105:452-459(1999).
 DR EMBL; AJ243279; CAB45925.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 3 SR 4

RESULT 49

Q9XSQ4

ID Q9XSQ4 PRELIMINARY; PRT; 11 AA.
 AC Q9XSQ4;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain (Fragment).

GN PDGFA.
 OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
 OX NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20065871; PubMed=10598812;
 RA Bonthron D.T., Smith S.L., Campbell R.;
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."
 RL Hum. Genet. 105:452-459(1999).
 DR EMBL; AJ243278; CAB45916.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1F2D4 CRC64;

Query Match 18.2%; Score 2; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 3 SR 4

RESULT 50

O77900

ID O77900 PRELIMINARY; PRT; 11 AA.
 AC O77900;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci."
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050010; AAC41349.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4

Db

||
8 SR 9

RESULT 51

O77917

ID O77917 PRELIMINARY; PRT; 11 AA.
AC O77917;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050030; AAC41369.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4

||

Db 8 SR 9

RESULT 52

O77902

ID O77902 PRELIMINARY; PRT; 11 AA.
AC O77902;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;

RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050012; AAC41351.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 8 SR 9

RESULT 53

O77921

ID O77921 PRELIMINARY; PRT; 11 AA.
 AC O77921;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS Pseudotropheus sp. 'Pseudotropheus tropheops complex'.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
 OC Cichlidae; Pseudotropheus.
 OX NCBI_TaxID=51796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050034; AAC41373.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 8 SR 9

RESULT 54

Q9TQB3

ID Q9TQB3 PRELIMINARY; PRT; 11 AA.
AC Q9TQB3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class I related protein 1 (Fragment).
GN MR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98451457; PubMed=9780177;
RA Riegert P., Wanner V., Bahram S.;
RT "Genomics, isoforms, expression, and phylogeny of the MHC class I-
RT related MR1 gene.";
RL J. Immunol. 161:4066-4077(1998).
DR EMBL; AF039526; AAD02172.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1235 MW; 5E71A31E29CDD697 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 4 LM 5

RESULT 55
O77901

ID O77901 PRELIMINARY; PRT; 11 AA.
AC O77901;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050011; AAC41350.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 8 SR 9

RESULT 56

077892

ID 077892 PRELIMINARY; PRT; 11 AA.
AC 077892;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 10 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050002; AAC41341.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1277 MW; 74855B73786B572B CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
||
Db 9 SL 10

RESULT 57

077916

ID 077916 PRELIMINARY; PRT; 11 AA.
AC 077916;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050029; AAC41368.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 8 SR 9

RESULT 58

O77885

ID O77885 PRELIMINARY; PRT; 11 AA.
 AC O77885;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 4 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF049994; AAC41333.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1253 MW; 72325B701EA5B72B CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10

Db ||
 9 SL 10

RESULT 59

O77905

ID O77905 PRELIMINARY; PRT; 11 AA.
AC O77905;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci."
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050015; AAC41354.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
Db 8 SR 9

RESULT 60

O77884

ID O77884 PRELIMINARY; PRT; 11 AA.
AC O77884;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 4 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;

RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF049993; AAC41332.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1253 MW; 72325B701EA5B72B CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
 ||
 Db 9 SL 10

RESULT 61
 O77906

ID O77906 PRELIMINARY; PRT; 11 AA.
 AC O77906;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 1 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050016; AAC41355.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1277 MW; 74855B73786B572B CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
 ||
 Db 9 SL 10

RESULT 62
 O77899

ID O77899 PRELIMINARY; PRT; 11 AA.
AC O77899;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci."
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050009; AAC41348.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 8 SR 9

RESULT 63

O77918
ID O77918 PRELIMINARY; PRT; 11 AA.
AC O77918;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 1 (Fragment).
OS Pseudotropheus sp. 'Pseudotropheus tropheops complex'.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Pseudotropheus.
OX NCBI_TaxID=51796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci."
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050031; AAC41370.1; -.

FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1320 MW; 74855B69C86B572B CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
||
Db 9 SL 10

RESULT 64

O77893

ID O77893 PRELIMINARY; PRT; 11 AA.
AC O77893;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 10 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci."
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050003; AAC41342.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1296 MW; 68775B73786B572B CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
||
Db 9 SL 10

RESULT 65

O78121

ID O78121 PRELIMINARY; PRT; 11 AA.
AC O78121;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 12 (Fragment).

OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050027; AAC41366.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1362 MW; 03C12D8EB7341B54 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 8 SR 9

RESULT 66

O77904

ID O77904 PRELIMINARY; PRT; 11 AA.
 AC O77904;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050014; AAC41353.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 8 SR 9

RESULT 67

O77903

ID O77903 PRELIMINARY; PRT; 11 AA.
AC O77903;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid mhc
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050013; AAC41352.1; -.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 8 SR 9

RESULT 68

O77913

ID O77913 PRELIMINARY; PRT; 11 AA.
AC O77913;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 4 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98315113; PubMed=9649539;
 RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 RT class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050024; AAC41363.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1181 MW; 72325B737EA5B72B CRC64;

Query Match 18.2%; Score 2; DB 7; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
 ||
 Db 9 SL 10

RESULT 69

Q9G5Y6

ID Q9G5Y6 PRELIMINARY; PRT; 11 AA.
 AC Q9G5Y6;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Agama agama (Red-headed rock agama).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae; Agama.
 OX NCBI_TaxID=103336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128504; AAG00749.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1324 MW; 9D52EC1E336415A1 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
||
Db 5 SR 6

RESULT 70

Q8MEL7

ID Q8MEL7 PRELIMINARY; PRT; 11 AA.
AC Q8MEL7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Sida hookeriana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Sida.
OX NCBI_TaxID=108446;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384624; AAM50396.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RK 5
||
Db 6 RK 7

RESULT 71

Q9G5Y0

ID Q9G5Y0 PRELIMINARY; PRT; 11 AA.
AC Q9G5Y0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Pseudotrapelus sinaitus.
OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Agaminae;
 OC Pseudotrapelus.
 OX NCBI_TaxID=118229;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic
 RT structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128507; AAG00758.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1374 MW; B05439FE336415B6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SR 4
 ||
 Db 5 SR 6

RESULT 72

Q8MEM2

ID Q8MEM2 PRELIMINARY; PRT; 11 AA.
 AC Q8MEM2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Lagunaria patersonia.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Lagunaria.
 OX NCBI_TaxID=183274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron.";
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384616; AAM50388.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RK 5
||
Db 6 RK 7

RESULT 73

Q8MES5

ID Q8MES5 PRELIMINARY; PRT; 11 AA.
AC Q8MES5;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein 16 (Fragment).
GN RPL16.
OS Abelmoschus manihot.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Abelmoschus.
OX NCBI_TaxID=183220;
RN [1]
RP SEQUENCE FROM N.A.
RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT chloroplast DNA sequences of ndhF and the rpl16 intron."
RL Syst. Bot. 27:333-350(2002).
DR EMBL; AF384561; AAM50399.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RK 5
||
Db 6 RK 7

RESULT 74

Q8WD17

ID Q8WD17 PRELIMINARY; PRT; 11 AA.
AC Q8WD17;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Ctenophorus reticulatus (Western netted dragon).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Amphibolurinae;
 OC Ctenophorus.
 OX NCBI_TaxID=180002;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Melville J., Schulte J.A. II, Larson A.;
 RT "A molecular phylogenetic study of ecological diversification in the
 RT Australian lizard genus Ctenophorus."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF375634; AAL40433.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1313 MW; A8F7371E336415B6 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SR 4
 ||
 Db 5 SR 6

RESULT 75

Q9G368

ID Q9G368 PRELIMINARY; PRT; 11 AA.
 AC Q9G368;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Draco blanfordii.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Agamidae; Draconinae;
 OC Draco.
 OX NCBI_TaxID=89021;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97153820; PubMed=9000751;
 RA Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Replication slippage may cause parallel evolution in the secondary
 RT structures of mitochondrial transfer RNAs."
 RL Mol. Biol. Evol. 14:30-39(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114082; PubMed=12118408;
 RA Macey J.R., Schulte J.A. II, Larson A.;
 RT "Evolution and information content of the mitochondrial genomic

RT structural features illustrated with acrodont lizards."
 RL Syst. Biol. 49:257-277(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22114081; PubMed=12118407;
 RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Wang Y.,
 RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.;
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 RT phylogenetics."
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL; AF128477; AAG00668.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1341 MW; 4B2D371E336415B7 CRC64;

Query Match 18.2%; Score 2; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 5 SR 6

Search completed: April 8, 2004, 15:46:10
 Job time : 28.7692 secs

OM protein - protein search, using sw model

Run on: April 8, 2004, 15:30:07 ; Search time 5.15385 Seconds
 (without alignments)
 111.135 Million cell updates/sec

Title: US-09-787-443A-21
 Perfect score: 11
 Sequence: 1 AKSRKGNSSLM 11

Scoring table: OLIGO
 Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 70

Minimum DB seq length: 11
 Maximum DB seq length: 11

Post-processing: Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3	27.3	11	1	Q2OA_COMTE	P80464 comamonas t
2	2	18.2	11	1	BRK_MEGFL	P12797 megascolia
3	2	18.2	11	1	CORZ_PERAM	P11496 periplaneta
4	2	18.2	11	1	HS70_PINPS	P81672 pinus pinas
5	2	18.2	11	1	NXSN_PSETE	P59072 pseudonaja
6	2	18.2	11	1	OAIF_SARBU	P83518 sarcophaga
7	2	18.2	11	1	RS30_ONCMY	P83328 oncorhynchu
8	2	18.2	11	1	TKC2_CALVO	P41518 calliphora
9	2	18.2	11	1	TKN1_PSEGU	P42986 pseudophryn
10	2	18.2	11	1	TKN1_UPEIN	P82026 uperoleia i
11	2	18.2	11	1	TKN1_UPERU	P08612 uperoleia r
12	2	18.2	11	1	TKN2_PSEGU	P42987 pseudophryn
13	2	18.2	11	1	TKN2_UPERU	P08616 uperoleia r
14	2	18.2	11	1	TKN3_PSEGU	P42988 pseudophryn
15	2	18.2	11	1	TKN4_PSEGU	P42989 pseudophryn
16	2	18.2	11	1	TKN5_PSEGU	P42990 pseudophryn
17	2	18.2	11	1	TKNA_CHICK	P19850 gallus gall

18	2	18.2	11	1	TKNA_GADMO	P28498	gadus morhu
19	2	18.2	11	1	TKNA_HORSE	P01290	equus cabal
20	2	18.2	11	1	TKNA_ONCMY	P28499	oncorhynchu
21	2	18.2	11	1	TKNA_RANCA	P22688	rana catesb
22	2	18.2	11	1	TKNA_RANRI	P29207	rana ridibu
23	2	18.2	11	1	TKNA_SCYCA	P41333	scyliorhinu
24	2	18.2	11	1	TKN_ELEMO	P01293	eledone mos
25	2	18.2	11	1	TKN_PHYFU	P08615	physalaemus
26	2	18.2	11	1	UXB2_YEAST	P99013	saccharomyc
27	1	9.1	11	1	ANGT_CRIGE	P09037	crinia geor
28	1	9.1	11	1	ASL1_BACSE	P83146	bacteroides
29	1	9.1	11	1	ASL2_BACSE	P83147	bacteroides
30	1	9.1	11	1	BPP3_BOTIN	P30423	bothrops in
31	1	9.1	11	1	BPP4_BOTIN	P30424	bothrops in
32	1	9.1	11	1	BPPB_AGKHA	P01021	agkistrodon
33	1	9.1	11	1	BPP_AGKHP	P04562	agkistrodon
34	1	9.1	11	1	CA21_LITCI	P82087	litoria cit
35	1	9.1	11	1	CA22_LITCI	P82088	litoria cit
36	1	9.1	11	1	CA31_LITCI	P82089	litoria cit
37	1	9.1	11	1	CA32_LITCI	P82090	litoria cit
38	1	9.1	11	1	CA41_LITCI	P82091	litoria cit
39	1	9.1	11	1	CA42_LITCI	P82092	litoria cit
40	1	9.1	11	1	CEP1_ACHFU	P22790	achatina fu
41	1	9.1	11	1	COXA_CANFA	P99501	canis famil
42	1	9.1	11	1	CSI5_BACSU	P81095	bacillus su
43	1	9.1	11	1	CX5A_CONAL	P58848	conus aulic
44	1	9.1	11	1	CX5B_CONAL	P58849	conus aulic
45	1	9.1	11	1	CXL1_CONMR	P58807	conus marmo
46	1	9.1	11	1	EFG_CLOPA	P81350	clostridium
47	1	9.1	11	1	ES1_RAT	P56571	rattus norv
48	1	9.1	11	1	FAR6_PENMO	P83321	penaeus mon
49	1	9.1	11	1	FAR9_CALVO	P41864	calliphora
50	1	9.1	11	1	LADD_ONCMY	P81018	oncorhynchu
51	1	9.1	11	1	LPW_THETH	P05624	thermus the
52	1	9.1	11	1	LSK1_LEUMA	P04428	leucophaea
53	1	9.1	11	1	LSKP_PERAM	P36885	periplaneta
54	1	9.1	11	1	MHBI_KLEPN	P80580	klebsiella
55	1	9.1	11	1	MLG_THETS	P41989	theromyzon
56	1	9.1	11	1	MORN_HUMAN	P01163	homo sapien
57	1	9.1	11	1	NUHM_CANFA	P49820	canis famil
58	1	9.1	11	1	PKC1_CARMO	P82684	carausius m
59	1	9.1	11	1	PQQC_PSEFL	P55173	pseudomonas
60	1	9.1	11	1	PVK1_PERAM	P41837	periplaneta
61	1	9.1	11	1	RANC_RANPI	P08951	rana pipien
62	1	9.1	11	1	RE41_LITRU	P82074	litoria rub
63	1	9.1	11	1	RR2_CONAM	P42341	conopholis
64	1	9.1	11	1	RRPL_CHAV	P13179	chandipura
65	1	9.1	11	1	T2P1_PROVU	P31031	proteus vul
66	1	9.1	11	1	TIN1_HOPTI	P82651	hoplobatrac
67	1	9.1	11	1	TIN4_HOPTI	P82654	hoplobatrac
68	1	9.1	11	1	TKND_RANCA	P22691	rana catesb
69	1	9.1	11	1	UF05_MOUSE	P38643	mus musculu
70	1	9.1	11	1	ULAG_HUMAN	P31933	homo sapien

ALIGNMENTS

RESULT 1

Q2OA_COMTE

ID Q2OA_COMTE STANDARD; PRT; 11 AA.
AC P80464;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinoline 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuaka B., Fetzner S., Lingens F.;
RT "Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -!- FUNCTION: Converts (3-methyl-)-quinoline to (3-methyl-)2-oxo-
CC 1,2-dihydroquinoline.
CC -!- CATALYTIC ACTIVITY: Quinoline + acceptor + H(2)O = isoquinolin-
CC 1(2H)-one + reduced acceptor.
CC -!- COFACTOR: FAD, molybdenum and iron-sulfur.
CC -!- PATHWAY: Degradation of quinoline and (3-methyl-)quinoline; first
CC step.
CC -!- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and
CC two gamma chains (Probable).
DR PIR; S66606; S66606.
KW Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1213 MW; 869094322B1DC2CA CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKS 3
|||
Db 1 AKS 3

RESULT 2

BRK_MEGFL

ID BRK_MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Megascoliakinin ([Thr6]bradykinin-Lys-Ala) [Contains: Bradykinin-like
DE peptide ([Thr6]bradykinin)].
OS Megascolia flavifrons (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;

OC Scoliididae; Megascolia.
 OX NCBI_TaxID=7437;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=87293024; PubMed=3617088;
 RA Yasuhara T., Mantel P., Nakajima T., Piek T.;
 RT "Two kinins isolated from an extract of the venom reservoirs of the
 RT solitary wasp *Megascolia flavifrons*.";
 RL Toxicon 25:527-535(1987).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Nakajima T., Piek T., Yashuara T., Mantel P.;
 RT "Two kinins isolated from the venom of *Megascolia flavifrons*.";
 RL Toxicon 26:34-34(1988).
 CC -!- FUNCTION: Both proteins have bradykinin-like, although lower
 CC activities (e.g. smooth muscle contraction).
 CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -!- SIMILARITY: Belongs to the bradykinin family.
 DR PIR; B26744; B26744.
 DR GO; GO:0005615; C:extracellular space; IDA.
 DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.
 DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.
 KW Bradykinin; Vasodilator.
 FT PEPTIDE 1 11 MEGASCOLIAKININ.
 FT PEPTIDE 1 9 BRADYKININ-LIKE PEPTIDE.
 SQ SEQUENCE 11 AA; 1273 MW; 33867393D771A9C8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RK 5
 ||
 Db 9 RK 10

RESULT 3

CORZ_PERAM
 ID CORZ_PERAM STANDARD; PRT; 11 AA.
 AC P11496;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Corazonin.
 OS *Periplaneta americana* (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; *Periplaneta*.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=89325572; PubMed=2753132;
 RA Veenstra J.A.;
 RT "Isolation and structure of corazonin, a cardioactive peptide from

RT the American cockroach.";
 RL FEBS Lett. 250:231-234(1989).
 CC -!- FUNCTION: Cardioactive peptide. Corazonin is probably involved
 CC in the physiological regulation of the heart beat.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1387 MW; C7CFF32D6415AB46 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SR 4
 ||
 Db 6 SR 7

RESULT 4

HS70_PINPS

ID HS70_PINPS STANDARD; PRT; 11 AA.
 AC P81672;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Heat shock 70 kDa protein (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
 CC (spot N164) is: 5.4, its MW is: 73 kDa.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 KW ATP-binding; Heat shock; Multigene family.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1228 MW; 037C1BE8DAA44DD0 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GN 7
 ||
 Db 9 GN 10

RESULT 5

NXSN_PSETE

ID NXSN_PSETE STANDARD; PRT; 11 AA.
 AC P59072;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Short neurotoxin N1 (Alpha neurotoxin) (Fragment).
 OS Pseudonaja textilis (Eastern brown snake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophiinae; Pseudonaja.
 OX NCBI_TaxID=8673;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99449602; PubMed=10518793;
 RA Gong N.L., Armugam A., Jeyaseelan K.;
 RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
 RT cloning, expression and protein characterization.";
 RL Eur. J. Biochem. 265:982-989(1999).
 CC -!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
 CC acetylcholine receptors (nAChR).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -!- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.
 CC -!- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
 CC -!- SIMILARITY: Belongs to the snake toxin family.
 DR InterPro; IPR003571; Snake_toxin.
 DR PROSITE; PS00272; SNAKE_TOXIN; PARTIAL.
 KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
 KW Acetylcholine receptor inhibitor; Multigene family.
 FT UNSURE 3 3
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1319 MW; 0D1EF0C81B58732B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 KG 6
 ||
 Db 5 KG 6

RESULT 6

OAIF_SARBU

ID OAIF_SARBU STANDARD; PRT; 11 AA.
 AC P83518;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ovary-derived ACE interactive factor (Neb-ODAIF) [Contains: Neb-
 DE ODAIF(1-9); Neb-ODAIF(1-7)].
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND MASS SPECTROMETRY.
 RC TISSUE=Ovary;
 RX MEDLINE=22272747; PubMed=12383874;
 RA Vandingenen A., Hens K., Baggerman G., Macours N., Schoofs L.,
 RA De Loof A., Huybrechts R.;
 RT "Isolation and characterization of an angiotensin converting enzyme
 RT substrate from vitellogenic ovaries of *Neobellieria bullata*."
 RL Peptides 23:1853-1863(2002).
 CC -!- FUNCTION: Substrate for angiotensin converting enzyme (ACE) in
 CC vitro.
 CC -!- PTM: ACE hydrolyzes Neb-ODAIF by sequentially cleaving off two C-
 CC terminal dipeptides.
 CC -!- MASS SPECTROMETRY: MW=1312.7; METHOD=MALDI; RANGE=1-11.
 CC -!- SIMILARITY: To the N-terminal part of insect vitellogenins.
 FT PEPTIDE 1 11 NEB-ODAIF.
 FT PEPTIDE 1 9 NEB-ODAIF(1-9).
 FT PEPTIDE 1 7 NEB-ODAIF(1-7).
 SQ SEQUENCE 11 AA; 1314 MW; 4E114BB566C5A763 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 SL 10
 ||
 Db 10 SL 11

RESULT 7

RS30_ONCMY

ID RS30_ONCMY STANDARD; PRT; 11 AA.
 AC P83328;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 40S ribosomal protein S30 (Fragment).
 GN FAU.
 OS Oncorhynchus mykiss (Rainbow trout) (*Salmo gairdneri*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Skin mucus;
 RX MEDLINE=22142142; PubMed=12147245;
 RA Fernandes J.M.O., Smith V.J.;
 RT "A novel antimicrobial function for a ribosomal peptide from rainbow
 RT trout skin."
 RL Biochem. Biophys. Res. Commun. 296:167-171(2002).
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive
 CC bacteria.
 CC -!- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.

CC -!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.
KW Ribosomal protein; Antibiotic.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 SL 10
 ||
Db 5 SL 6

RESULT 8

TKC2_CALVO
ID TKC2_CALVO STANDARD; PRT; 11 AA.
AC P41518;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Callitachykinin II.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX MEDLINE=95075727; PubMed=7984492;
RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
RA Naessel D.R.;
RT "Callitachykinin I and II, two novel myotropic peptides isolated from
RT the blowfly, Calliphora vomitoria, that have resemblances to
RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: Myoactive peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDD444 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GN 7
 ||
Db 3 GN 4

RESULT 9

TKN1_PSEGU
ID TKN1_PSEGU STANDARD; PRT; 11 AA.
AC P42986;
DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-I (PG-KI).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylaidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; B60409; B60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1269 MW; 3DBA7C37C9CB1AB7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LM 11
 ||
 Db 10 LM 11

RESULT 10

TKN1_UPEIN

ID TKN1_UPEIN STANDARD; PRT; 11 AA.
 AC P82026;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperin 1.1.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylaidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.

OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 RT floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
 ||
 Db 10 LM 11

RESULT 11

TKN1_UPERU

ID TKN1_UPERU STANDARD; PRT; 11 AA.
 AC P08612;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperolein.
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=75131227; PubMed=1120493;
 RA Anastasi A., Erspamer V., Endean R.;
 RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
 RT in the skin of Uperoleia rugosa and Uperoleia marmorata.";
 RL Experientia 31:394-395(1975).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,

CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LM 11
 ||
 Db 10 LM 11

RESULT 12

TKN2_PSEGU

ID TKN2_PSEGU STANDARD; PRT; 11 AA.
 AC P42987;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kassinin-like peptide K-II (PG-KII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guntheri."
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; C60409; C60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.

DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1246 MW; 3A247C37C9CB1AB7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
 ||
 Db 10 LM 11

RESULT 13

TKN2_UPERU

ID TKN2_UPERU STANDARD; PRT; 11 AA.
 AC P08616;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Rugosauperolein II ([Lys5,Thr6]physalaemin).
 OS Uperoleia rugosa (Wrinkled toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=8368;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=80223080; PubMed=7389029;
 RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;
 RT "Physalaemin- and bombesin-like peptides in the skin of the
 RT Australian leptodactylid frog Uperoleia rugosa."
 RL Chem. Pharm. Bull. 28:689-695(1980).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 14

TKN3_PSEGU

ID TKN3_PSEGU STANDARD; PRT; 11 AA.
AC P42988;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kassinin-like peptide K-III (PG-KIII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; D60409; D60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1268 MW; 3DBA7C37C9CB1457 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 15

TKN4_PSEGU

ID TKN4_PSEGU STANDARD; PRT; 11 AA.
 AC P42989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P-like peptide I (PG-SPI).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; E60409; E60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LM 11
 ||
 Db 10 LM 11

RESULT 16

TKN5_PSEGU

ID TKN5_PSEGU STANDARD; PRT; 11 AA.
 AC P42990;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P-like peptide II (PG-SPII).
 OS Pseudophryne guentheri (Guenther's toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Pseudophryne.
 OX NCBI_TaxID=30349;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90287814; PubMed=2356157;
 RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
 RA Roberts J.D., Melchiorri P., Erspamer V.;
 RT "Six novel tachykinin- and bombesin-related peptides from the skin of
 RT the Australian frog Pseudophryne guentheri.";
 RL Peptides 11:299-304(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; F60409; F60409.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LM 11
 ||
 Db 10 LM 11

RESULT 17

TKNA_CHICK

ID TKNA_CHICK STANDARD; PRT; 11 AA.
 AC P19850;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;

RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=88204263; PubMed=2452461;
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
 RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
 RL Regul. Pept. 20:171-180(1988).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; JN0023; JN0023.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LM 11
 ||
 Db 10 LM 11

RESULT 18

TKNA_GADMO

ID TKNA_GADMO STANDARD; PRT; 11 AA.
 AC P28498;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Gadus morhua (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
 OX NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout.";
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; S23306; S23306.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
 ||
 Db 10 LM 11

RESULT 19

TKNA_HORSE

ID TKNA_HORSE STANDARD; PRT; 11 AA.
 AC P01290;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Equus caballus (Horse), and
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796, 10141;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Horse;
 RA Studer R.O., Trzeciak A., Lergier W.;
 RT "Isolation and amino-acid sequence of substance P from horse
 RT intestine.";
 RL Helv. Chim. Acta 56:860-866(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.porcellus;
 RX MEDLINE=90044685; PubMed=2478925;
 RA Murphy R.;
 RT "Primary amino acid sequence of guinea-pig substance P.";
 RL Neuropeptides 14:105-110(1989).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A01558; SPHO.
 DR PIR; A60654; A60654.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.

DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
 ||
 Db 10 LM 11

RESULT 20

TKNA_ONCMY

ID TKNA_ONCMY STANDARD; PRT; 11 AA.
 AC P28499;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout."
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S23308; S23308.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 21

TKNA_RANCA

ID TKNA_RANCA STANDARD; PRT; 11 AA.
AC P22688;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ranatachykinin A (RTK A).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain, and Intestine;
RX MEDLINE=91254337; PubMed=2043143;
RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT brain and intestine.";
RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN [2]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=94023216; PubMed=8210506;
RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT intestine.";
RL Regul. Pept. 46:81-88(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; A61033; A61033.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 22

TKNA_RANRI

ID TKNA_RANRI STANDARD; PRT; 11 AA.
 AC P29207;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranakinin (Substance-P-related peptide).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92044543; PubMed=1658233;
 RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
 RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
 RT neurokinin B from the brain of the frog Rana ridibunda."
 RL J. Neurochem. 57:2086-2091(1991).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
 ||
 Db 10 LM 11

RESULT 23

TKNA_SCYCA

ID TKNA_SCYCA STANDARD; PRT; 11 AA.
 AC P41333;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.

OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=93292508; PubMed=7685693;
 RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;
 RT "Primary structures and biological activities of substance-P-related
 RT peptides from the brain of the dogfish, *Scyliorhinus canicula*.";
 RL Eur. J. Biochem. 214:469-474(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S33300; S33300.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LM 11
 ||
 Db 10 LM 11

RESULT 24

TKN_ELEMO

ID TKN_ELEMO STANDARD; PRT; 11 AA.
 AC P01293;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Eledoisin.
 OS Eledone moschata (Musky octopus) (*Ozaena moschata*), and
 OS Eledone cirrhosa (Curled octopus) (*Ozaena cirrosa*).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Eledone.
 OX NCBI_TaxID=6641, 102876;
 RN [1]
 RP SEQUENCE.
 RA Anastasi A., Erspamer V.;
 RT "The isolation and amino acid sequence of eledoisin, the active
 RT endecapeptide of the posterior salivary glands of Eledone."
 RL Arch. Biochem. Biophys. 101:56-65(1963).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.

DR PIR; A01561; EEOC.
 DR PIR; B01561; EEOCC.
 DR PDB; 1MXQ; 18-FEB-03.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Pyrrolidone carboxylic acid;
 KW 3D-structure.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1206 MW; 570D7C2559CDDAA3 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
 ||
 Db 10 LM 11

RESULT 25

TKN_PHYFU

ID TKN_PHYFU STANDARD; PRT; 11 AA.
 AC P08615;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Physalaemin.
 OS Physalaemus fuscumaculatus (Neotropical frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
 OC Leptodactylinae; Physalaemus.
 OX NCBI_TaxID=8378;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=66076612; PubMed=5857249;
 RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;
 RT "Structure and pharmacological actions of physalaemin, the main
 RT active polypeptide of the skin of Physalaemus fuscumaculatus.";
 RL Experientia 20:489-490(1964).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S07201; S07201.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LM 11
||
Db 10 LM 11

RESULT 26

UXB2_YEAST

ID UXB2_YEAST STANDARD; PRT; 11 AA.
AC P99013;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page (Spot 2D-000K2F) (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RC STRAIN=X2180-1A;
RA Sanchez J.-C., Golaz O., Schaller D., Morch F., Frutiger S.,
RA Hughes G.J., Appel R.D., Deshusses J., Hochstrasser D.F.;
RL Submitted (AUG-1995) to Swiss-Prot.
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.20, its MW is: 9.2 kDa.
DR SWISS-2DPAGE; P99013; YEAST.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1328 MW; EC38021C0DCB42DA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RK 5
||
Db 8 RK 9

RESULT 27

ANGT_CRIGE

ID ANGT_CRIGE STANDARD; PRT; 11 AA.
AC P09037;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Crinia-angiotensin II.
OS Crinia georgiana (Quacking frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Crinia.
OX NCBI_TaxID=8374;
RN [1]

RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=80024575; PubMed=488254;
 RA Erspamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
 RT "Amino acid composition and sequence of crinia-angiotensin, an
 RT angiotensin II-like endecapeptide from the skin of the Australian
 RT frog *Crinia georgiana*.";
 RL Experientia 35:1132-1133(1979).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 DR PIR; S07207; S07207.
 KW Vasoconstrictor.
 SQ SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 1 A 1

RESULT 28

ASL1_BACSE

ID ASL1_BACSE STANDARD; PRT; 11 AA.
 AC P83146;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acharan sulfate lyase 1 (EC 4.2.2.-) (Fragment).
 OS Bacteroides stercoris.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=46506;
 RN [1]
 RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
 RC STRAIN=HJ-15;
 RX MEDLINE=21223019; PubMed=11322884;
 RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
 RT "Purification and characterization of acharan sulfate lyases, two
 RT novel heparinases, from *Bacteroides stercoris* HJ-15.";
 RL Eur. J. Biochem. 268:2635-2641(2001).
 CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
 CC heparin and heparan sulfate.
 CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and cobalt.
 CC Activated by reducing agents, such as DL-dithiothreitol and 2-
 CC mercaptoethanol.
 CC -!- SUBUNIT: Monomer.
 CC -!- PTM: The N-terminus is blocked.
 CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
 CC 7.2 and optimum temperature 45 degrees Celsius.
 KW Lyase; Heparin-binding.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1395 MW; 01B2DAA241E865AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 N 7
|
Db 1 N 1

RESULT 29

ASL2_BACSE

ID ASL2_BACSE STANDARD; PRT; 11 AA.
AC P83147;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 2 (EC 4.2.2.-) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=46506;
RN [1]
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN=HJ-15;
RX MEDLINE=21223019; PubMed=11322884;
RA Kim B.-T., Hong S.-W., Kim W.-S., Kim Y.S., Kim D.-H.;
RT "Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HJ-15."
RL Eur. J. Biochem. 268:2635-2641(2001).
CC -!- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate.
CC -!- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.
CC Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC -!- SUBUNIT: Monomer.
CC -!- PTM: The N-terminus is blocked.
CC -!- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1195 MW; D79D897C7AA451AD CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
|
Db 4 A 4

RESULT 30

BPP3_BOTIN

ID BPP3_BOTIN STANDARD; PRT; 11 AA.
AC P30423;
DT 01-APR-1993 (Rel. 25, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,3,2 (10C) (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; C37196; C37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1199 MW; 20B25813C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
 |
 Db 3 G 3

RESULT 31

BPP4_BOTIN

ID BPP4_BOTIN STANDARD; PRT; 11 AA.
 AC P30424;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from Bothrops insularis snake venom.";
 RL J. Protein Chem. 9:221-227(1990).

CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; D37196; D37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1143 MW; 20BBBF13C7741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
 |
 Db 2 G 2

RESULT 32

BPPB AGKHA

ID BPPB AGKHA STANDARD; PRT; 11 AA.
 AC P01021;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide B (Angiotensin-converting
 DE enzyme inhibitor).
 OS Agkistrodon halys blomhoffii (Mamushi) (Gloydus blomhoffii).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydus.
 OX NCBI_TaxID=242054;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Kato H., Suzuki T.;
 RT "Amino acid sequence of bradykinin-potentiating peptide isolated from
 RT the venom of Agkistrodon halys blomhoffii."
 RL Proc. Jpn. Acad., B, Phys. Biol. Sci. 46:176-181(1970).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR; A01254; XASNBA.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
 |
 Db 2 G 2

RESULT 33

BPP_AGKHP

ID BPP_AGKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water mocassin) (Gloydus halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydus.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide
RT from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; JC0002; XAVIBH.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
|
Db 2 G 2

RESULT 34

CA21_LITCI

ID CA21_LITCI STANDARD; PRT; 11 AA.
AC P82087;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 2.1/2.1Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;

RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 2.1Y4 differs from isoform 2.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1372; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1312 MW; 10DAB7C4EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
 |
 Db 6 G 6

RESULT 35

CA22_LITCI

ID CA22_LITCI STANDARD; PRT; 11 AA.
 AC P82088;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 2.2/2.2Y4.
 OS *Litoria citropa* (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; *Litoria*.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog *Litoria citropa*. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 2.2Y4 differs from isoform 2.2 in not being

CC sulfated.
 CC -- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
 CC -- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB894EDD861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
 |
 Db 6 G 6

RESULT 36

CA31_LITCI

ID CA31_LITCI STANDARD; PRT; 11 AA.
 AC P82089;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 3.1/3.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -- SUBCELLULAR LOCATION: Secreted.
 CC -- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -- PTM: Isoform 3.1Y4 differs from isoform 3.1 in not being
 CC sulfated.
 CC -- MASS SPECTROMETRY: MW=1407; METHOD=Electrospray.
 CC -- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1347 MW; 10DAB7D67861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
|
Db 5 G 5

RESULT 37

CA32_LITCI

ID CA32_LITCI STANDARD; PRT; 11 AA.
AC P82090;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Caerulein 3.2/3.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC Pelodryadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
RT mountains tree frog Litoria citropa. Part 1. Sequence determination
RT using electrospray mass spectrometry."
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC -!- PTM: Isoform 3.2Y4 differs from isoform 3.2 in not being
CC sulfated.
CC -!- MASS SPECTROMETRY: MW=1423; METHOD=Electrospray.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 4 4 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1363 MW; 10DAB8867861A86B CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
|
Db 5 G 5

RESULT 38

CA41_LITCI

ID CA41_LITCI STANDARD; PRT; 11 AA.
 AC P82091;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 4.1/4.1Y4.
 OS Litoria citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodyadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 4.1Y4 differs from isoform 4.1 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1388; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1328 MW; 10DAB7C4F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
 |
 Db 6 G 6

RESULT 39

CA42_LITCI

ID CA42_LITCI STANDARD; PRT; 11 AA.
 AC P82092;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 4.2/4.2Y4.
 OS Litoria citropa (Australian blue mountains tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT montains tree frog Litoria citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry."
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -!- FUNCTION: Hypotensive neuropeptide (Probable).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being
 CC sulfated.
 CC -!- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro; IPR001651; Gastrin.
 DR PROSITE; PS00259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 4 4 SULFATION.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 G 6
 |
 Db 6 G 6

RESULT 40

CEP1_ACHFU

ID CEP1_ACHFU STANDARD; PRT; 11 AA.
 AC P22790;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Cardio-excitatory peptide-1 (ACEP-1).
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
 OX NCBI_TaxID=6530;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Ferussac; TISSUE=Heart atrium;
 RX MEDLINE=90211261; PubMed=2322251;
 RA Fujimoto K., Ohta N., Yoshida M., Kubota I., Muneoka Y., Kobayashi M.;
 RT "A novel cardio-excitatory peptide isolated from the atria of the
 RT African giant snail, Achatina fulica."

RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
 CC -!- FUNCTION: Potentiates the beat of the ventricle, and has also
 CC excitatory actions on the penis retractor muscle, the buccal
 CC muscle and the identified neurons controlling the buccal muscle
 CC movement of achatina.
 CC -!- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
 DR PIR; A34662; A34662.
 KW Hormone; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1305 MW; 82D6D5B9C7741365 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 S 3
 |
 Db 1 S 1

RESULT 41

COXA_CANFA

ID COXA_CANFA STANDARD; PRT; 11 AA.
 AC P99501;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
 GN COX5A.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- FUNCTION: This is the heme A-containing chain of cytochrome c
 CC oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
 DR HSC-2DPAGE; P99501; DOG.
 DR InterPro; IPR003204; Cyt_c_ox5A.
 DR Pfam; PF02284; COX5A; 1.
 KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 S 3
|
Db 1 S 1

RESULT 42

CSI5_BACSU

ID CSI5_BACSU STANDARD; PRT; 11 AA.
AC P81095;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cold shock protein CSI5 (11 kDa cold shock protein) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / JH642;
RA Graumann P.L., Schmid R., Marahiel M.A.;
RL Submitted (OCT-1997) to Swiss-Prot.
RN [2]
RP CHARACTERIZATION.
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis."
RL J. Bacteriol. 178:4611-4619(1996).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: In response to low temperature.
CC -!- CAUTION: Could not be found in the genome of B.subtilis 168.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEE6322C330 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 R 4
|
Db 2 R 2

RESULT 43

CX5A_CONAL

ID CX5A_CONAL STANDARD; PRT; 11 AA.
AC P58848;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Conotoxin au5a.
OS Conus aulicus (Court cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89437;

RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99452958; PubMed=10521453;
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RT "The T-superfamily of conotoxins.";
 RL J. Biol. Chem. 274:30664-30671(1999).
 RN [2]
 RP ERRATUM.
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RL J. Biol. Chem. 274:36030-36030(1999).
 CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
 CC observed when injected into mice.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1436.6; METHOD=LSIMS.
 CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
 DR PIR; A59146; A59146.
 KW Toxin.
 FT DISULFID 2 9
 FT DISULFID 3 10
 SQ SEQUENCE 11 AA; 1441 MW; 21A36775440059D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 R 4
 |
 Db 7 R 7

RESULT 44

CX5B_CONAL

ID CX5B_CONAL STANDARD; PRT; 11 AA.
 AC P58849;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Conotoxin au5b.
 OS Conus aulicus (Court cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=89437;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=99452958; PubMed=10521453;
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RT "The T-superfamily of conotoxins.";

RL J. Biol. Chem. 274:30664-30671(1999).
 RN [2]
 RP ERRATUM.
 RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,
 RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,
 RA Bandyopadhyay P., Craig A.G., Olivera B.M.;
 RL J. Biol. Chem. 274:36030-36030(1999).
 CC -!- FUNCTION: Causes dorsal fins drooping in fish. No effect is
 CC observed when injected into mice (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1388.6; METHOD=LSIMS.
 CC -!- SIMILARITY: Belongs to the conotoxin T-superfamily.
 DR PIR; B59146; B59146.
 KW Toxin.
 FT DISULFID 2 9
 FT DISULFID 3 10
 SQ SEQUENCE 11 AA; 1393 MW; 21A36775440042D7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 R 4
 |
 Db 7 R 7

RESULT 45

CXL1_CONMR
 ID CXL1_CONMR STANDARD; PRT; 11 AA.
 AC P58807;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lambda-conotoxin CMrVIA.
 OS Conus marmoreus (Marble cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=20564325; PubMed=10988292;
 RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
 RA Seow K.T., Bay B.-H.;
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
 RT pattern and protein folding. Isolation and characterization from the
 RT venom of Conus marmoreus."
 RL J. Biol. Chem. 275:39516-39522(2000).
 CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
 KW Neurotoxin; Toxin; Hydroxylation.

FT DISULFID 2 11
 FT DISULFID 3 8
 FT MOD_RES 10 10 HYDROXYLATION.
 SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
 |
 Db 4 G 4

RESULT 46

EFG_CLOPA

ID EFG_CLOPA STANDARD; PRT; 11 AA.

AC P81350;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Elongation factor G (EF-G) (CP 5) (Fragment).

GN FUSA.

OS Clostridium pasteurianum.

OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

OC Clostridium.

OX NCBI_TaxID=1501;

RN [1]

RP SEQUENCE.

RC STRAIN=W5;

RX MEDLINE=98291870; PubMed=9629918;

RA Flengsrud R., Skjeldal L.;

RT "Two-dimensional gel electrophoresis separation and N-terminal
 sequence analysis of proteins from Clostridium pasteurianum W5.";

RL Electrophoresis 19:802-806(1998).

CC -!- FUNCTION: This protein promotes the GTP-dependent translocation of
 the nascent protein chain from the A-site to the P-site of the
 ribosome.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.

CC EF-G/EF-2 subfamily.

DR InterPro; IPR000795; EF_GTPbind.

DR PROSITE; PS00301; EFACOR_GTP; PARTIAL.

KW Elongation factor; Protein biosynthesis; GTP-binding.

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1337 MW; 412E71F1D9C33B17 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
 Db 1 K 1

RESULT 47

ES1_RAT

ID ES1_RAT STANDARD; PRT; 11 AA.
 AC P56571;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE ES1 protein, mitochondrial (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Heart;
 RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
 RA Jungblut P.R.;
 RL Submitted (SEP-1998) to Swiss-Prot.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
 CC -!- MISCELLANEOUS: By 2D-PAGE, the determined pI of this protein (spot
 CC P2) is: 8.9, its MW is: 25 kDa.
 CC -!- SIMILARITY: BELONGS TO THE ES1 FAMILY.
 KW Mitochondrion.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1142 MW; D862272D32C72DC2 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 R 4
 |
 Db 1 R 1

RESULT 48

FAR6_PENMO

ID FAR6_PENMO STANDARD; PRT; 11 AA.
 AC P83321;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide FLP6 (DGRTPALRLRF-amide).
 OS Penaeus monodon (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupuem J., Krungkasem C., Longyant S.,
 RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 RT of the giant tiger prawn Penaeus monodon."
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
 |
 Db 2 G 2

RESULT 49

FAR9_CALVO

ID FAR9_CALVO STANDARD; PRT; 11 AA.
 AC P41864;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CalliFMRFamide 9.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliFMRFamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR PIR; I41978; I41978.
 KW Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CAA44321 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 S 3
 |
 Db 1 S 1

RESULT 50

LADD_ONCMY

ID LADD_ONCMY STANDARD; PRT; 11 AA.
AC P81018;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Ladderlectin (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97293418; PubMed=9149391;
RA Jensen L.E., Thiel S., Petersen T.E., Jensenuis J.C.;
RT "A rainbow trout lectin with multimeric structure."
RL Comp. Biochem. Physiol. 116B:385-390(1997).
CC -!- FUNCTION: Lectin that binds sepharose.
CC -!- COFACTOR: Calcium is essential for sepharose binding.
CC -!- SUBUNIT: Multimeric.
KW Lectin; Calcium.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1163 MW; 0B26227FF6D45404 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 A 1
|
Db 1 A 1

RESULT 51

LPW_THETH

ID LPW_THETH STANDARD; PRT; 11 AA.
AC P05624;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Trp operon leader peptide.
GN TRPL.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=89000781; PubMed=2844259;
RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
RT HB8 trpE and trpG."
RL Biochim. Biophys. Acta 950:303-312(1988).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS

CC OF TRYPTOPHAN.

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CC -----
DR EMBL; X07744; CAA30565.1; -.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 M 11
|
Db 1 M 1

RESULT 52

LSK1_LEUMA

ID LSK1_LEUMA STANDARD; PRT; 11 AA.
AC P04428;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Leucosulfakinin-I (LSK-I).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RX MEDLINE=86315858; PubMed=3749893;
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
RT gastrin and cholecystokinin.";
RL Science 234:71-73(1986).
CC -!- FUNCTION: Change the frequency and amplitude of contractions of
CC the hingat. Inhibits muscle contraction of hindgut.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A01622; GMROL.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6 6 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 R 4
|
Db 10 R 10

RESULT 53

LSKP_PERAM

ID LSKP_PERAM STANDARD; PRT; 11 AA.
AC P36885;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Perisulfakinin (Pea-SK-I).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RX MEDLINE=90137190; PubMed=2615921;
RA Veenstra J.A.;
RT "Isolation and structure of two gastrin/CCK-like neuropeptides from
RT the American cockroach homologous to the leucosulfakinins.";
RL Neuropeptides 14:145-149(1989).
CC -!- FUNCTION: Stimulates hindgut contractions.
CC -!- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; A60656; A60656.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 6 6 SULFATION.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 R 4
|
Db 10 R 10

RESULT 54

MHBI_KLEPN

ID MHBI_KLEPN STANDARD; PRT; 11 AA.
AC P80580;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Maleylpyruvate isomerase (EC 5.2.1.4) (Fragment).
GN MHBI.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=573;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96349117; PubMed=8760924;
 RA Robson N.D., Parrott S., Cooper R.A.;
 RT "In vitro formation of a catabolic plasmid carrying Klebsiella
 RT pneumoniae DNA that allows growth of Escherichia coli K-12 on 3-
 RT hydroxybenzoate.";
 RL Microbiology 142:2115-2120(1996).
 CC -!- CATALYTIC ACTIVITY: 3-maleylpyruvate = 3-fumarylpyruvate.
 KW Isomerase.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1387 MW; 1EE0E2DD49C9D5AB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 M 11
 |
 Db 1 M 1

RESULT 55

MLG_THETS

ID MLG_THETS STANDARD; PRT; 11 AA.
 AC P41989;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
 OS Theromyzon tessulatum (Leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
 OX NCBI_TaxID=13286;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=94298944; PubMed=8026574;
 RA Salzet M., Wattez C., Bulet P., Malecha J.;
 RT "Isolation and structural characterization of a novel peptide related
 RT to gamma-melanocyte stimulating hormone from the brain of the leech
 RT Theromyzon tessulatum.";
 RL FEBS Lett. 348:102-106(1994).
 CC -!- SIMILARITY: Belongs to the POMC family.
 DR PIR; S45698; S45698.
 KW Hormone; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1486 MW; 2DB8FACE6409C1E8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 G 6
 |

RESULT 56

MORN_HUMAN

ID MORN_HUMAN STANDARD; PRT; 11 AA.
AC P01163;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Morphogenetic neuropeptide (Head activator) (HA).
OS Homo sapiens (Human),
OS Rattus norvegicus (Rat),
OS Bos taurus (Bovine),
OS Anthopleura elegantissima (Sea anemone), and
OS Hydra attenuata (Hydra) (Hydra vulgaris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
RN [1]
RP SEQUENCE.
RC SPECIES=Human, Rat, and Bovine;
RX MEDLINE=82035850; PubMed=7290191;
RA Bodenmuller H., Schaller H.C.;
RT "Conserved amino acid sequence of a neuropeptide, the head activator,
RT from coelenterates to humans.";
RL Nature 293:579-580(1981).
RN [2]
RP SEQUENCE.
RC SPECIES=A.elegantissima, and H.attenuata;
RA Schaller H.C., Bodenmuller H.;
RT "Isolation and amino acid sequence of a morphogenetic peptide from
RT hydra.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
RN [3]
RP SYNTHESIS.
RX MEDLINE=82050803; PubMed=7297679;
RA Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;
RT "Synthesis of a new neuropeptide, the head activator from hydra.";
RL FEBS Lett. 131:317-321(1981).
RN [4]
RP FUNCTION.
RX MEDLINE=90059923; PubMed=2583101;
RA Schaller H.C., Druffel-Augustin S., Dubel S.;
RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells
RT in the G2/mitosis transition.";
RL EMBO J. 8:3311-3318(1989).
CC -!- FUNCTION: HA acts as an autocrine growth factor for neural cells
CC in the G2/mitosis transition.
CC -!- CAUTION: This peptide was first isolated from nerve cells of hydra
CC and was called head activator by the authors, because it induced
CC head-specific growth and differentiation in this animal. It has
CC been found in mammalian intestine and hypothalamus.
DR PIR; A01427; YHRT.
DR PIR; A93900; YHXA.E.
DR PIR; B01427; YHHU.
DR PIR; B93900; YHJFHY.

DR PIR; C01427; YHBO.
 DR GK; P01163; -.
 KW Growth factor; Cell cycle; Mitosis; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
 |
 Db 4 G 4

RESULT 57

NUHM_CANFA

ID NUHM_CANFA STANDARD; PRT; 11 AA.
 AC P49820;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Fragment).
 GN NDUFV2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins."
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
 CC FRAGMENT OF THE ENZYME.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).
 CC -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
 CC -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
 CC mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
 DR HSC-2DPAGE; P49820; DOG.
 DR InterPro; IPR002023; Cmplx1_24kDa.
 DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
 KW Iron-sulfur; Iron; 2Fe-2S.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72DD8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
|
Db 1 G 1

RESULT 58

PKC1_CARMO

ID PKC1_CARMO STANDARD; PRT; 11 AA.
AC P82684;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-1 (Cam-PK-1) (FXPRL-Amide).
OS Carausius morosus (Indian stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;
OC Heteronemiidae; Carausius.
OX NCBI_TaxID=7022;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RA Predel R., Kellner R., Gaede G.;
RT "Myotropic neuropeptides from the retrocerebral complex of the stick
RT insect, Carausius morosus (Phasmatodea: Lonchodidae).";
RL Eur. J. Entomol. 96:275-278(1999).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro; IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 R 4
|
Db 10 R 10

RESULT 59

PQQC_PSEFL

ID PQQC_PSEFL STANDARD; PRT; 11 AA.
AC P55173;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Coenzyme PQQ synthesis protein C (Pyrroloquinoline quinone
DE biosynthesis protein C) (Fragment).
GN PQQC.

OS *Pseudomonas fluorescens*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; *Pseudomonas*.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHA0;
 RX MEDLINE=96064397; PubMed=8526497;
 RA Schnider U., Keel C., Defago G., Haas D.;
 RT "Tn5-directed cloning of pqq genes from *Pseudomonas fluorescens* CHA0:
 RT mutational inactivation of the genes results in overproduction of the
 RT antibiotic pyoluteorin.";
 RL Appl. Environ. Microbiol. 61:3856-3864(1995).
 CC -!- PATHWAY: Pyrroloquinoline quinone (PQQ) biosynthesis.
 CC -!- SIMILARITY: Belongs to the pqqC family.

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DR EMBL; X87299; CAA60734.1; -.
 DR PIR; S58244; S58244.
 DR HAMAP; MF_00654; -; 1.
 KW PQQ biosynthesis.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1182 MW; 89DF46E4C5B73771 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 M 11
 |
 Db 1 M 1

RESULT 60

PVK1_PERAM

ID PVK1_PERAM STANDARD; PRT; 11 AA.
 AC P41837;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Periviscerokinin-1 (Pea-PVK-1).
 OS *Periplaneta americana* (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
 OC Blattidae; *Periplaneta*.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Abdominal perisymphathetic organs;
 RX MEDLINE=95232021; PubMed=7716075;

RA Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
 RT "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
 RT perisymphatic organs of the American cockroach.";
 RL Peptides 16:61-66(1995).
 CC -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
 CC HYPERNEURAL MUSCLE.
 KW Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1114 MW; 39DB5419D7605728 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 G 6
 |
 Db 1 G 1

RESULT 61

RANC_RANPI

ID RANC_RANPI STANDARD; PRT; 11 AA.
 AC P08951;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatensin-C.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=84131098; PubMed=6141890;
 RA Nakajima T.;
 RL Unpublished results, cited by:
 RL Erspamer V., Erspamer G.F., Mazzanti G., Endean R.;
 RL Comp. Biochem. Physiol. 77C:99-108(1984).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the bombesin/neuromedin B/ranatensin
 CC family.
 DR InterPro; IPR000874; Bombesin.
 DR Pfam; PF02044; Bombesin; 1.
 DR PROSITE; PS00257; BOMBESIN; 1.
 KW Amphibian defense peptide; Bombesin family; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1304 MW; D6C9885A61ADC366 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 6 A 6

RESULT 62

RE41_LITRU

ID RE41_LITRU STANDARD; PRT; 11 AA.
 AC P82074;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Rubellidin 4.1.
 OS Litoria rubella (Desert tree frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Pelodryadinae; Litoria.
 OX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australin red tree frog
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians.";
 RL Aust. J. Chem. 49:955-963(1996).
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
 CC activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1039; METHOD=FAB.
 KW Amphibian defense peptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1040 MW; 84ED5CBC2877205A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 G 6
 |
 Db 1 G 1

RESULT 63

RR2_CONAM

ID RR2_CONAM STANDARD; PRT; 11 AA.
 AC P42341;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chloroplast 30S ribosomal protein S2 (Fragment).
 GN RPS2.
 OS Conopholis americana (Squawroot).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiids; Lamiales; Orobanchaceae; Orobancheae; Conopholis.
 OX NCBI_TaxID=4179;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92145776; PubMed=1723664;
 RA Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;
 RT "Lack of a functional plastid tRNA(Cys) gene is associated with loss
 RT of photosynthesis in a lineage of parasitic plants.";
 RL Curr. Genet. 20:515-518(1991).
 CC -!- SIMILARITY: Belongs to the S2P family of ribosomal proteins.
 CC -----
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 CC -----
 DR EMBL; X64567; CAA45868.1; -.
 DR PIR; S32575; S32575.
 DR HAMAP; MF_00291; -; 1.
 DR InterPro; IPR001865; Ribosomal_S2.
 DR PROSITE; PS00962; RIBOSOMAL_S2_1; PARTIAL.
 DR PROSITE; PS00963; RIBOSOMAL_S2_2; PARTIAL.
 KW Ribosomal protein; Chloroplast.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 M 11
 |
 Db 1 M 1

RESULT 64

RRPL_CHAV

ID RRPL_CHAV STANDARD; PRT; 11 AA.
 AC P13179;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
 DE (L protein) (Fragment).
 GN L.
 OS Chandipura virus (strain I653514).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Vesiculovirus.
 OX NCBI_TaxID=11273;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89299473; PubMed=2741347;
 RA Masters P.S., Bhella R.S., Butcher M., Patel B., Ghosh H.P.,
 RA Banerjee A.K.;
 RT "Structure and expression of the glycoprotein gene of Chandipura
 RT virus.";

RL Virology 171:285-290(1989).

CC -!- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
 CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPPING, AS WELL AS
 CC METHYLATION OF CAPS, AND POLY(A) SYNTHESIS.

CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA} (N).

CC -!- SUBUNIT: THOUGHT TO FORM A TRANSCRIPTION COMPLEX WITH THE
 CC NUCLEOCAPSID (N) PROTEIN.

CC -!- SIMILARITY: WITH THE L PROTEIN OF OTHER RHABDOVIRUSES AND
 CC PARAMYXOVIRUSES.

CC -----

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 CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; J04350; AAA42917.1; -.

KW Transferase; RNA-directed RNA polymerase.

FT NON TER 11 11

SQ SEQUENCE 11 AA; 1189 MW; 0335D6E3AAB2D764 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 M 11
 |
 Db 1 M 1

RESULT 65

T2P1_PROVU

ID T2P1_PROVU STANDARD; PRT; 11 AA.

AC P31031;

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)

DE (R.PvuI) (Fragment).

GN PVUIR.

OS Proteus vulgaris.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Proteus.

OX NCBI_TaxID=585;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 13315;

RX MEDLINE=93087186; PubMed=1454536;

RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;

RT "Cloning and characterization of genes for the PvuI restriction and
 RT modification system.";

RL Nucleic Acids Res. 20:5743-5747(1992).

CC -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
 CC CLEAVES AFTER T-4.

CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC specific double-stranded fragments with terminal 5'-phosphates.
CC -----
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CC -----
DR EMBL; L04163; AAA25660.1; -.
DR PIR; S35490; S35490.
DR REBASE; 1541; PvuI.
KW Restriction system; Hydrolase; Nuclease; Endonuclease.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1300 MW; 9F0CDE7955B72B1A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 S 3
 |
Db 2 S 2

RESULT 66

TIN1_HOPTI
ID TIN1_HOPTI STANDARD; PRT; 11 AA.
AC P82651;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tigerinin-1.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
FT DISULFID 2 10
FT MOD_RES 11 11 AMIDATION.

SQ SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 R 4
|
Db 9 R 9

RESULT 67

TIN4_HOPTI

ID TIN4_HOPTI STANDARD; PRT; 11 AA.
AC P82654;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tigerinin-4.
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;
OC Hoplobatrachus.
OX NCBI_TaxID=103373;
RN [1]
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Skin secretion;
RX PubMed=11031261;
RA Purna Sai K., Jaganadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitaram N.;
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 3 11
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 8.7e+04;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 R 4
|
Db 1 R 1

RESULT 68

TKND_RANCA

ID TKND_RANCA STANDARD; PRT; 11 AA.
AC P22691;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatachykinin D (RTK D).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
 RT brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=94023216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
 RT intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; D61033; D61033.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; FALSE_NEG.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 K 2
 |
 Db 1 K 1

RESULT 69

UF05_MOUSE

ID UF05_MOUSE STANDARD; PRT; 11 AA.
 AC P38643;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P48) (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE=95009907; PubMed=7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familiar and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.5, its MW is: 48 kDa.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1328 MW; E54835E5CAAABAFa CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 K 2
 |
 Db 1 K 1

RESULT 70

ULAG_HUMAN

ID ULAG_HUMAN STANDARD; PRT; 11 AA.
 AC P31933;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 118) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
 RA Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993.";
 RL Electrophoresis 14:1216-1222(1993).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.5, its MW is: 34 kDa.
 DR SWISS-2DPAGE; P31933; HUMAN.
 DR Siena-2DPAGE; P31933; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1219 MW; EDABD37F272DDB0A CRC64;

Query Match 9.1%; Score 1; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.7e+04;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 A 1
 |
 Db 6 A 6

Search completed: April 8, 2004, 15:47:24
Job time : 6.15385 secs